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Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF135028	RESULT 1
The new kallikrein-like gene, KLK-L2. Molecular characterization, mapping, tissue expression, and hormonal regulation	Yousef, G.M. and Diamandis, E.P.	1 (bases 1 to 11570)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AF135028.1 GI:4589282	AF135028	Homo sapiens kallikrein-like protein 2 KLK-L2 gene, complete cds.	AF135028 11570 bp DNA linear PRI 27-JUN-2000		

Pred. No. is the number of results predicted by chance to have a

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Yousef,G.M., Luo,L.Y. and
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Sinal Hospital, 600 Unive
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Diamandis, E.P., Yousef, G.
The new human kallikrein
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/protein_id="AAD56429.1"
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/translation="MATARPPMMWVLCALITALLLGVTEHVLANNDVSCDHPSNTVPS
/translation="MATARPPMMWVLCALITALLLGVTEHVLANNDVSCDHPSNTVPS
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LLTAANGRKYVERVRLGHYSLSPVYESGQOMPGOGVKSIPHPGYSHPGHSDLMLIKNG
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/product="kallikrein-like protein 2
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/mol_type="genomic DNA"
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AC011483
AC011483.7
                                                  Direct Submission
Submitted (01-JUL-2002) DOE Joint Genome Institute, 2800 M
Drive, Walnut Creek, CA 94598, USA
On Jul 1, 2002 this sequence version replaced gi:14971176.
Draft Sequence Produced by DOE Joint Genome Institute
WWW.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.6.
NOTE: Shatter libraries failed to resolve dinucleotide repeat.
                                                                                                                                                       DOE
                                                                                                                                                              Direct Submission
Submitted (07-OCT-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (bases 1 to 107487)
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Mammalia; Eutheria; Primates;
1 (bases 1 to 107487)
DOE Joint Genome Institute and
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Submitted
Bothell, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230000
Homo sapiens serine protease
AF243527
AF243527.1 GI:11244757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 257
20510030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gan,L., Lee,I., Smith,R., A. Moss,P., Paeper,B. and Wang Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gan,L., Lee,I., Smith,R., Argonza-Barrett,R., Lei
Moss,P., Paeper,B. and Wang,K.
Sequencing and expression analysis of the serine
cluster located in chromosome 19q13 region
Gene 257 (1), 119-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 230000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1054574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTCTAGTTGAACCCTGGGAACAATTTCCAAAACTGTCCAGGGCGGGGGTTGCGTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAATTTAGTCCCAGAAATAAACTGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCTCCCTGGGGCACTTTCATCCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (human)
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                                  /product="ACO protease" complement(join(13552. 15416. .15569,19204. .1.
                                                                                           IEPENFSFPDDLQCVDLKILPNDECKKAHVQKVTDFMLCVGHLEGGKDTCVGDSGGPLMCDGVLQGVTSGKYVPCGTPNKPSVAVEVLSYVKMIEDTIAENS*
complement(join(<13552. 13704,14377. .14530,14678. .14917
15416. .15569,19204. .>19246))
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fstfqcggilvhrqwvltaahcisdnyqlwlgrhnlfddentaqfvhvsesfphpgfn
msllenhtrqadedyshdlmllrltepadtitdavkvvelpteepevgstclasgwgs
                                                                                                                                                                                                                                                                                                                                  /gene="KLK1"
/product="renal kallikrein"
complement(join(6963. .7118,7668.
9482. .9641,11472. .11517))
                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(<6963. .>11517)
/gene="KLK1"
                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(<6963. .7118,7668. 9482. .9641,11472. .>11517))
                                                                                                                                                                                                                                                                                                   /gene="KLK1"
/note="serine protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                             /protein_id="AAG33353.1"
/db_xref="GI:11244758"
                                                                                                                                                                                                                                                              /product="renal kallikrein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="19q13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
/codon_start=1
                     /note="serine
                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (09-MAR-2000) Chiroscience
VA 98021, USA
                 protease"
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ng,K.
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gene
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                                      19246))
                                                          .13704,14377.
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                                                          .14530,
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                                                            ,14678.
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                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MWVPVVFLTLSVTWIGAAPLILSRIVGGWECEKHSQPWQVLVAS RGRAVCGGVLVHPQWVLTAAHCIRNKSVILLGHSLEHPEDTGQVFQVSHSEPHPLYD MSLLKNRFLRPEDDSSHDLMLLRLSEPAELTDAVKVMDLPTQEPALGTTCYASGWGSI EPEEFLIPKKLQCVDLHVISNIVCAQVHPQKVTKFMLCAGRWTGGKSTCSGDSGPLV CNGVLQGITSWGSEPCALPERPSLYTKVVHYRKWIKDTIVANP"
                                                                                                                                                                                                                               complement(join(<131301. .131456,136310.
136529. .136785,137525. .137690,140255.</pre>
                                                                                                                                                                                                                                                                                                                                MPTVLQCVNVSVVSEEVCSKLYDPLYHPSMFCAGGGHDQKDSCNGDSGGPLICNGYLQ
GLVSFGKAPCGQVGVPGVYTNLCKFTEWIEKTVQAS"
complement(<131301. .>140303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP"
complement(join(<94602. .94754,96027. .96163,96247. .96497
96919. .97081,98345. .>98405))
                                                                                                                                                                                                                                                                                                                                                                                                        /translation="matagnpwgwflgylilgyagslysgscsqlingedcsphsopw
QaalvwenelfcsgylvhpQwvlsaahcfQnsytiglglhsleadqepgsqwveasls
VRHPEYNRPLLANDLMLIKLDESVSESDTIRSISIASQCPTAGNSCLYSGwGLLANGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96919. .97081,98345. .98405))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="serine protease"
complement(join(94602...94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:11244761"
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/translation="MWDLVLSIALSVGCTGAVPLIQSRIVGGWECEKHSQPWQVAVYS
HGWAHCGGVLVHPQWVLTAAHCLKKNSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYN
MSLLKHQSLRPDEDSSHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUTANS 18 ti On="1WHLLLTLSFLLASTAAQDGDKLLEGDECAPHSQPWQVALYERGR
FNCGASLISHWYLSAAHCQSBEMRVRLGEHNLRKRDGFEQLETTSRVLIPHFRYEARS
HRNDIMLLRLVQPARLNPQVRPAVLFDTRCPHGEACYVSGWGLVPLSSPVSLDDTLLG
ANISIISDTSCDKSYPGRLTNTMVCAGAEGRGAESCEGDSGGPLVCGGILQGIVSWGD
     /product="stratum corneum trypsin-likė serine protease"
/protein_id="AAG33358.1"
/db_xref="GI:11244763"
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/db_xref="GI:11244762"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPEEFLRPRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="glandular kallikrein"
join(61139. .61184,62391. .6255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="prostate specific antigen"
/protein_id="AAG33355.1"
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/db_xref="GI:11244759"
                                                                                                                                                                                                                                                                                   /note="synonym: SCTE"
                                                                                                                                                                                                                                                                                                        /gene="KLK5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="serine protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="KLK2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(<61139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="KLK2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="prostate
join(42595. .42640,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="KLK3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               )oin(<42595.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="serine protease"
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                                                                                   codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="serine protease"
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                                                                                                                                                                                                                               .>140303))
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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     100.0%;
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complement(join(183943. .184098,185635. .185768, 187865. .188127,188293. .188452,188967. .189036)
//note="serine protease; also called ovasin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: SCCE"
complement(join(<165420. .165575,167672. .167808,
168124. .168371,169651. .169798,170211. .>170283))
                                                                                                                                                                                                                                                                                                                                                                                                    DGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKKIIGSKG"
complement(join(<190980. 191129,191573. 1g
194324. 194589,197048. 197204,197370. .>19
/product="kallikrein-like 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQ
SIPHPCYNSSDVEDHNHDLMLLQLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(<183943. .184098,185635. 187865. .188127,188293. .188452,188967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYSTQTHVNDLMLVKLNSQARLSSMYKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFP
SDLMCVDVKLISPQDCTKVYKDLLENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGL
VSWGTFPCGQPNDPGVYTQVCKFTKWINDTMKKHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="stratum corneum chymotryptic enzyme"
complement(join(165420. .165575,167672. .167808,
168124. .168371,169651. .169798,170211. .170283))
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GSKEKPGVYTNVCRYTNWIQKTIQAK"
complement(<165420. .>170283)
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151186. .151433,155052. .155208,155948. .155987))
/note="serine protease; also called neurosin or z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGYSHPGHSNDLMLIKLNRRIRPTKDYRPINVSSHCPSAGTKCLVSGWGTTKSPQVHF
PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCNGSLQGL
VSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS"
TLQCANISILENKLCHWAYPGHISDSMLCAGLWEGGRGSCQGDSGGPLVCNGTLAGVV
SGGAEPCSRPRRPAVYTSVCHYLDWIQEIMEN"
                                                            /translation="MKLGLLCALLSLLAGHGWADTRAIGAEECRPNSQPWQAGLFHLT
RLFCGATLISDRWLLTAAHCRKPYLWVRLGEHHLWKWEGPEQLFRVTDFFPHPGFNKD
LSANDHNDDIMLIRLPRQARLSPAVQPLNLSQTCVSPGMQCLISGWGAVSSPKALFPV
                                                                                                                                                                                                                                                                                                                                    complement(join(190980..191129,191573..191709, 194324..194589,197048..197204,197370..197412))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="neuropsin"
/protein_id="AAG33361.1"
/db_xref="GI:11244766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VALLSGNQLHCGGVLVNERWVLTAAHCKMNEYTVHLGSDTLGDRRAQRIKASKSFRHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="stratum corneum chymotryptic enzyme"
/protein_id="AAG33360.1"
/db_xref="GI:11244765"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(<146834...146986,149628.
151186...151433,155052...155208,155948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAGSSKGADTCQGDSGGPLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mkKLMVVLSLIAAAWAEEQNKLVHGGPCDKTSHPYQAALYTSGH
LLCGGVLIHPLWVLTAAHCKKPNLQVFLGKHNLRQRESSQEQSSVVRAVIHPDYDAAS
HDQDIMLLRLARPAKLSELIQPLPLERDCSANTTSCHILGWGKTADGDFPDTIQCAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="protease M"
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/db_xref="GI:11244764"
                                                                                                                                                                  /protein_id="AAG33362.1"
/db_xref="GI:11244767"
                                                                                                                                                                                                                                     /product="kallikrein-like
                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                             note="serine protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQ"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="neuropsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MARSLLLPLQILLLSLALETAGEEAQGDKIIDGAPCARGSHPWQ/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="KLK7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="KLK7"
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.>155987))
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Score 2071; Pred. No. 0

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OY 1021 AAGAGGAAGATGGAGTGAAAATGGGGTCTAAAGGTTGAACTTGGAGGCCAGG 1080	Qy         901         GGCGGAGAGATACACGATGAGGGAGACAGGCTGGAACAGAAAGTAGAGACGAAGATTCGA         960           ll	132268 841 132208	721 ALCAGOLICAGA DECEMBRISCO DE CONSTRUCCIÓN D	661 TGCCAAGTGTGCTGTTCAACATGCTATGATGCACACGGCAGGCCTCCACAACAACCATT 7	601 GGAGACATTITTGGTTGTCACAACTATATGGAGGGGCATTACTGGAACTAATGGATAGA 	541 TCCAAGCGAATGGATTCTATTGGGAGTGATTCTGCCCCTAGAAGACACTGGCAATACCA 600	13240 GAGGAAGGAATTATAGGGGGGAAGTATGGGGAATTGAAGACAGGAACACAAATTAG 540 481 TATTATAGGAGGGTAATTATAGGGGAGGTATGGGGAATTGAAGACAGGAAACACAAATTAG 540	13200 GAARGAAAGGAAGGAAGGAAAGGAAAGGAAAAAAAAAA	361 GAAAGAAAGGAAAGAAAGAAAAGAAAAGAAAGAAAGAA	132808	241 CAAAGCAAGACGTTTTTGTCAGAAAGAAAAAAAAAAAGAGACGAAGGGAGGAGGAGAGAG 300	181 CGTTTGAGGCTGCGGTAAGCCATGACTGCACTGCACTCCAGACAGCAGCCTGGGTGA 240	121 132928	132988	y 1 AAACAGACCAAAAACTTCCTGCCGCGTGGACCTCATGTTCCCCAAGTGGAAGACAGGCAA 60 	Matches 2071; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULACO27	אַ עַם מּם.	Db Qy	Db Qy Db	Oy Oy	Qy	. Qy	Qy	Qy	Qy Db	Qy Db	ДУ	ДУ	Оу	Db	da Q	 ?
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AC027602				ACTCCTGAG	CGGGTGTCT/          CGGGTGTCT/	ATGGCTCCCT	GCCTCTCTC!	TCCATCTATO	TTTTCTGCAT	AGTGAAATAJ            AGTGAAATAJ	GCGCTCCAAC	GGCAGGAGAA              GGCAGGAGAA	ACAAAAAATT	GGCCAGGAGT	CATGGTGGCT	o saccionation of the sacc
	GECCAGAAA GTCCCAGAAA GTCCCAGAAA	TGAACCCTGG            TGAACCCTGG	TTTCAGACCC CCATGTCTCC IIIIIIIIIII	TCATCCCAGG	ACACGAACCT          ACACGAACCT	TGCAGGGACT	ATGCCCCCCT          ATGCCCCCCT	GGCATCTCT           GGCATCTCT	TTTCTTCATC	PTAATAACAT:             TAATAACAT:	CTGGGCAAC!	ATTGCTTGAAC	PAGCCGGGTGT	TCGAGACCAC	CACGCCIGIA	, , , , , , , , , , , , , , , , , , ,
217346 bp		GAACAATTTC	TCATTCCTTCC TGGACTCAGG	ACTCAGCACACACACACACACACACACACACACACACACA	CTGCAAGTTC!          CTGCAAGTTC!	CGTGTCCTGG           CGTGTCCTGG	TTCTCTCCTGC	GGGTCTCTCAN 	CTGTACTTTC	CTCCCTCTCT CTCCCTCTCT	AGAGTAAGACT                       AGAGTAAGACT	CCGGGAGATO	GGTGATGGAC	CCTGGCCAAC	HICCCAACAC	DATION A COOTE
DNA	TCAGGGCCCA TCAGGGCCCA AG 2071    	CAAAACTGTC             CAAAACTGTC	CAGAGATGT TCTGCTTCC	CCGGCATCCC CCGGCATCCC CCGGCATCCC CCAGAGATGT	ACCAAGTGGA ACCAAGTGGA	GAGATTACO	CAGGGTGATT                     CAGGGTGATT	GTCTCCTTC	CATCTCTGT           CATCTCTGT	CTCCTTTTG	CCATCTCAA	GAGGCTGCA	ACCTGTAGTO	ATGGTGAAAC	TTTGGAGGCT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
linear	HIIIIIII	CAGGGCGGG	TGAGAATGT	CACCTGCTGC               CACCTGCTGC  TGAGAATGTT	TCCAGGAAAC	CTTGTGCCCC	CTGGGGGGC           CTGGGGGGC	TGCCCACTT	GTGTCTGTT         GTGTCTGTT	CCTGTGTCT          CTGTGTCT	AAAAAAAA            \AAAAAAA	GTGAGCTGA         	CACAGCTAC	COCETCIO 111111111111111111111111111111111111	GAGGTGGG	JOSSOFT STATE
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REFERENCE
AUTHORS
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Grand, S., Grand, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I. Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Volung, G., Zainoun, T., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connoř, T.,
O'Donnell, P., O'Neil, D., Ollara, T.M., Ollver, J., Peterson, K.,
Plerre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graham, L., Grand-Fierre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G. Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE,
AC027602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Choepellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 217346)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Calpoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodde,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG;
                                                                                                                                                                                                                                                                                                                                                   Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                            Nov 15, 2000 this sequence version replaced repeats were identified using RepeatMasker. t, A.F.A. & Green, P. (1996-1997)
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Contact: sequence_submissions@genome.wi.mit.edu
                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                          Center code: WIBR
                                                                                                                                               Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens chromosome 19 clone.RP11-795B6 map 19, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 unordered pieces.
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Eutheria; Primates;
                                                                                                                                                                                 Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nusbaum, C. and Lander, E. me 19, clone RP11-795B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     replaced gi:11136831
                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abraham, H., Allen, N.
                                                                                                                                            Genome
                                                                                                                                               Research
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9693. .10733

10834

.13519

17611

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9592

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assembly\_fragment"

vector\_side:left" clone\_end:SP6

note="assembly\_fragment

clone\_lib="RPCI-11 Human Male BAC"

/clone="RP11-795B6"

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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 194000; agarose-fp
Insert size: 216246; sum-of-contigs
Quality coverage: 11.9 in Q20 bases; agarose-fp
Quality coverage: 10.7 in Q20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 210748 bases at least Q40 Consensus quality: 213655 bases at least Q30 Consensus quality: 215058 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; M77815; 31% of reads Sequencing vector: Plasmid; n/a; 69% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: 795_B_6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8150
8250
                                      /mol_type="genomic
                                                        /organism="Homo sapiens"
/chromosome="19"
                      /db_xref="taxon:9606"
                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                       gap
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193123 1860 193063 1920 193003	Qy Qy GG	194203 ATCCAGCTTCAGATGCCCAGATGCCCAGTGCCCAGTGCATCCAGGGAACCCTCATCCAGGGGCTGAGAAC 194144  781 CGTATTTTGCCAGAAGGGAGGTATAAGGATGGGTTGGTGGAGAATGGGGAAGGAAGGTGT 840	Q
1740 AACTCCTGAGTCATCCCAGGACTCAGCACACCGGCATCCCACCTGCTGCAGGACAGCCCACCTGCTGCAGGACCAGCACCACCTGCTGCAGGACCAGCACCAGCACCAGCACCAGCACCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCCCAATCCATCC	оу Оу Оу	661 TGCCAAGTGTTGTTCAACATGCTATGATGCACAGGCAGGC	0y 0y
1680 163243	Qy Db	194383 TCCAAGCGAATGGATTCTATTGGGAGTGATTCTGCCCTAGAAGACACTGCAATACCA 194324  601 GGAGACATTTTGGTTGACAACTAFATGGAGGGGCATTACTGGCCAACTAATGGATAGA 660	D O D
193 193	Oy Db	481 TATTATAGGAGGGTAATTATAGGGAGGTATGGGGAATTGAAGACACAAATTAG. 540	Qy Qy
1500 193 <b>4</b> 23	Оу	194563 GAAAGAAAGGAAAGAAAAGAAAAGAAAAAAAAAAAAA	p 0 p
193543 GAGTGAAATATTAATAACATTCTCCCTCTCTCTCTTTTGCCTGTGTCTCCATCTCTGTC  193543 GAGTGAAATATTAATAACATTCTCCCTCTCTCTCTCTTTTGCCTGTGTCTCTCCATCTCTGTCT  1440 TTTTTCTGCATTTCTTCATCTCTGTACTTTCCATCTCTGTGTGTCTGTC	рь 2у рь	301 AAAGGAAGGAAGGAAAGGAAAGGAAGGAAGGAAGGAAG	\$ \$ \$ \$
1321 193603 1380	Оу Оу	241 CAAAGCAAGACGTTTTTGTCAGAAAGAAAAAAAAAAAGAGACGAAGGGAAGGAA	g Qy
7 1261 GGCAGGAGAATTGCTTGAACCCGGGAGATGGAGGCTGCAGTGAGCTGAGGTCAGGCCACT	Qy	181 CGTTTGAGGCTGCGGTAAGCCATGACTGCACTGCTGCACTCCAGACAGCAGCCTGGGTGA 240	Dy S
7 1201 ACAAAAATTAGCCGGGTGTGGTGATGACACCTGTAGTCACAGCTACTTGGGAGGCTGA	Qy db	121 CTTGCACCTGTAGTTCCAGCTACTTGGGAGGCTGAGGTGGGAGAATTGCTTGAGCCCAAA 180	P &
7 1141 GGCCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACAAAAAAAT	Фр	61 TAAAGAGATAAATATGTAGTAAATTAAAAAAAAAAAAA	ρ Q
7 1081 CATGGTGGCTCACGCCTGTAATCCCAACACTTTGGAGGCTGAGGTGGGCGAATCACTTGA 	Qy Db	1 AAACAGACCAAAAAACTICCIGCCGCGTGGACCICATGTICCCCAAGTGGAAGACAGGCAA 60	P Q
1021 AAGAGGAAGATGGAGTGGAGAGTGACAAATGGGGTCTAAAGGTTGAACTTGGAGGCCAGG 	Оу	Note: Match 96.1%; Score 1990; DB 2; Length 217346; Best Local Similarity 98.7%; Pred. No. 0; Matches 2045; Conservative 0; Mismatches 5; Indels 22; Gaps 3;	,
961 GATGTGGAGAGGGAAGGGTCACAGACCCCCCGAAATGATGTGTGGACAACAGGAATCTGG	Qy Db	CALORE, ENGLY TA CALORE, ENGLY TA CALORE, ENGLY TA Vector_side:right"  BASE COUNT 55109 a 54154 c 53923 g 53053 t 1107 others  ORIGIN	о m
901 GGCGGAGAGATACACGATGAGGGAGACAGGCTGGAACAGAAAGTAGAGAGAG	Qy	misc_feature 163444, 208917  misc_feature 209018, 217346  misc_feature 209018, 217346	
194083 GTGTCCAGTAAGAGAAATAAGGCCTGCACAGGCTGGAGGGGAGAGTGAGAGAGA	Db	misc_feature 134765162343	

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REFERENCE
AUTHORS
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AC130782/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                             The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2040 CCCAAATTTAGTCCCAGAAATAAACTGAGAAG 2071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benjamin, B., Blakesley, R. W., Bouffard, G.G., Brinkley, C., Brooks, S. Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J. W., Thomas, P.J., Touchman, J. W., Vogt, J.L. Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (22-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Nov 22, 2002 this sequence version replaced gi:22218452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 200792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (chimpanzee)
Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akhter, N., Antonellis, A., Ayele, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC130782.2 GI:25167101
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Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly Program: Phrap; version 0.990319 consensus quality: 196656 bases at least Q40 consensus quality: 197883 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
Center project name: dhz
Center clone name: 355A20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: NIH Intramural Sequencing Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J.,
                                                                                                                                                             -- Summary Statistics
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by the finished sequence as soon as it is available and the accession number will be preserved.

1 28306: contig of 28306 bp in length 28307 28406: gap of unknown length 28407 37856: contig of 9450 bp in length 37857 37956: gap of unknown length 37857 37956: gap of unknown length 37957 73522: contig of 35566 bp in length 73523 73622: gap of unknown length 73523 38367: contig of 9945 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consists of 12 contigs. Gap are represented as runs of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is believed of the gaps
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193445. .199363
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                                                                                                                                                                                                            'note="assembly_fragment"
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159879: contig of 34168 bp in length
159979: gap of unknown length
174698: contig of 14719 bp in length
174798: gap of unknown length
18482: contig of 11584 bp in length
186482: gap of unknown length
193344: contig of 6862 bp in length
193344: gap of unknown length
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88817: contig
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. Qy	δ δ	Db Qy	Db Qy	Од	Db Qy	Оy	ОУ	Ωу	Оy	DЬ	Q. V	Ş 8	Qy Db	D 04	Db .	O E	P Qy	Qy Db	Query Best 1 Match	BASE COUNT ORIGIN
961	901 G	841 ( 68950 (	781 (	721 <i>1</i> 69070 <i>1</i>	661 T	601 (	541 : 69250 :	481 : 69310 :	421 G       69370 G	69373		301 /	241 C     69431 C	181 C     69491 C	51	121 C	61	1 <i>1</i> 69667 <i>1</i>	Match Local S es 1907	
ATGTGGA	GCGGAGA	STGTCCAG STGTCCAG	CGTATTTT         GTATTTC	ATCCAGCT ATCCAGCT	GCCAAGT	GAGACAT          GAGACAT	CCAAGCG	PATTATAG           ATTATAG	BAGGAAGG           BAAGAAGG		BAAAGAAA	\AAGGAAG	CAAAGCAA                 CAAAGCAA	CGTTTGAG	TTACACC	TTGCACC	TAAAGAGA	VAACAGAC          VAACAGAC	imilarity ; Conserva	49975 a
GAGGAAGG	GATACACO	TAAGAGAA                   TAAGAGAA	TGCAGAAG          TGCAGAAG	TCAGATGC	GTGCTGTT         GTGCTGTT	TTTTGGTT         TTTTGGTT	AATGGATT          AATGGATT	GAGGGTAA         GAGGGTAA	AAGGAAAG        AAGGAAGG		GGAAGAAA	GAAGGAAG	GACGTTTT         GAACTTTT	GCTGCGGT	TGTAGTTC	TGTAGTTC	TAAAGAGATAGATAAATATGTAGTAAATTA	CAAAAACT          CAAAAACT	81. 92. tive	49805 с
GTCACAG	ATGAGGGA	ATAAGGCC	GGAGGTAI	CCACAGTO	CAACATGO	GTCACAAC	TCTATTGO	TTATAGGO	AAGGAAAJ           AAGGAAAJ		.GAGAAAG <i>I</i>	GAGAAAG!	TGTCAGA!          TGTCAGA!	AAGCCATC	CAGCTACT	CAGCTACT	TATGTAG	TCCTGCC	4%; Scor 0%; Prec	48502
 	AGACAGGC	CTGCACAG CTGCACAG	FAAGGATG         FAAGGATG	SCCCAGATO SCCCAGATO	CTATGATG	TATATGG	GAGTGAT	SAGGTATG         SAGGTATG	AGAGGGAA.           AGAGGGAA.	1	aagaaaa.	AAAGGAAG	AAGAAAAA          AAG-AAAA	BACTGCACT BACAGCACT	TGGGAGG	TGGGAGG	FAAATTAA	SCGTGGAC	Score 1686.8; Pred. No. 0; 0; Mismatches	g 51409
ATGTGGAGAGGAAGGGTCACAGACCCCCCGAAATGATGTGTGGACAACAGGAATCTGG	GCGGAGAGATACACGATGAGGGAGACAGGCTGGAACAGAAAGTAGAGACGAAGATTCGA 	GTGTCCAGTAAGAGAAATAAGGCCTGCACAGGCTGGAGGGGAGAGTGAGAGAGA	CGTATTTTTGCAGAAGGAAGGTATAAGGATGGGTTGGTGGAGAATGGGGAAGGAAGGTG	ATCCAGCTTCAGATGCCCACAGTGCCCAGATCGAGGAACCCTCATCCAGGGGGTGAGAAC	TGCCAAGTGTGCTGTTCAACATGCTATGATGCACACGGCAGGCCTCCACAACAAACCATT 	GGAGACATTTTTGGTTGTCACAACTATATGGAGGGGCATTACTGGCAACTAATGGATAGA	TCCAAGCGAATGGATTTCTATTGGGAGTGATTCTGCCCCTAGAAGACACTGGCAATACCA	TATTATAGGAGGGTAATTATAGGGAGGTATGGGGAATTGAAGACAGGAAACACAAATTAG	aggaaggaaggaaggaaagaaagagggaaaaaatgactgttgaagagcagtgagtat 		aragaarggaagaargaaagaaagaaagaaagaaagaaa	aaaggaaggaaggaaaggaaaggaaggaaggaaagaaa	AAAGCAAGACGTTTTTGTCAGAAAGAAAAAAAAAAGAGGAGGAAGGGAGGAAGGA	CGTTTGAGGCTGCGGTAAGCCATGACTGCACTGCACTCCAGACAGCAGCCTGGGTGA 		aangagarah agataan atu tagtagatag tagagagagagaan taggcagggcaaa Tiggagcigigagatocaag tagagagaggcigagagagagaan taggcigagagagagagaa	AAAGAGATAGATAAATATGTAGTAAATTAAAAAAAAAA	AAACAGACCAAAAACTTCCTGCCGCGTGGACCTCATGTTCCCCAAGTGGAAGACAGGCAA	DB 2	9 t 1101
STGTGGAC	AAAGTAGA 	GGAGAGTG         GGAGAGTG	GAGAATGG          GAGAATGG	CCTCATCC          CCTCATCC	AGGCCTCC         AGGCCTCC	TACTGGCA         TACTGGCA	TAGAAGAC         TAGAAGAC	AAGACAGG          AGGACAGG	CTGTTGAA          CTGTTGAA		AGAAAGAA	AAGAAAGG.	ACGAAGGG.          ACGAAGGG	TCCAGACA	GAGAATT	SGAGAATTI	AAAAAATTAGCC	CCCCAAGT	; Length Indels	01 other
AACAGGAA	GACGAAGA	AGAGAGAA         AGAGAGAA	GGAAGGAA          GGAAGGAA	AGGGGCTG         AGGGGCTG	ACAACAAA          ACAACAAA	ACTAATGG         ACTAATGG	ACTGGCAA            ACTGGCAA	AAACACAA           AAACACAA	GAGCAGTG         GAGCAGTG		gaaagaaa	AAGGAAGG	AGGAAGGA         AGGAAGGG	GCAGCCTG        GCAGCCTG	GCTTGAGO	-aaaaaaaaattageeaggtgtgt Tgaggtgggagaattgettgageeeaaa	CCGGGTGTGGTGG	GGAAGACA           GGAAGACA	20079; 128;	v.
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CCAAATTI           CCAAATTI	ATCTCCC	CTCTCTAC	CTCTCTAC	TGACACTO	HCTCCTG!	CGGGTGTC	ACGGCTCC	GCCTCTCT	TCCATCTA	TCCATCTA	TTTTCTGC	AGTGAAAT	GCGCTCA		GGCAGGAG	ACAAAAA	IIIIIIII	HIIII II	ATGGTGG	ATGTGGAG
CCAAATTTAGTCCCAGAAATAAACTGAGAAG                       CCAAATTTAGTCCCAGAAATAAACTGAGAAG	ANICICCI DEGECACIIICA ICCICAMENICA DEGECCATCCCTTCTCTGCAGCTCTGA 		TCTCTCTAGTTGAACCCTGGGAACAATTTCCAAAACTGTCCAGGGCGGGGGTTGCGTCTC		ARCITOTION INTO CONSTRUCTION OF THE PROPERTY O	CCGGGTGTCTRCACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGC  -  -  -  -  -  -  -  -  -  -  -  -  -	ARIBOCITOCITOCINOBANICIONI CITUDOBANALIA COLLI DI SUCCESSIVO CORROCANO A CALLO			TGGGCATO	TITITCTGCATTTCTTCATCTCTGTACTTTCCATCTCTGTGTGTG	GAGTGAAATATTAATAACATTCTCCCTCTCTCTTTTTGCCTGTCTCTCTC	TAGESCA A A TA RETA A DE A ACASTROTOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOC		TTAGCCGG	TACAAAAAATTAGCCGGGTGTGGTGGTGGACACCTGTAGTCACAGCTACCTTGGGAGGCTG	GGCCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACAAAAAAAA		TATAGGTTGGCTTCACGCCTGTTAATTCCCAACACTTTTGGAGGTCGAGGTGGGGCGAATCACTTTGA	GATGTGGAGAGGAAGGGTCACAG-GCCCCCGAAATGATGTGT-GACAACAGGAATCTGG GATGTGGAGAGATGTGGAGAGAGTGACAAATGGGGTCTAAAGGTTGAACTTGGAGGAATCTGG
AAATAAA(          AAATAAA(	TTCATCC	TGGGAAC	TCCAGGACA	TOTTGEAC	I	COTOTO CA	ACTCGTGT	CCTTTCTC	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TCTGGGT	ATCTCTG	CATTCTCC	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		GAACCCGG	GTGTGGTG	CAGCCTGC	GTAATCC	GAGAGTGA	TCACAG-G
TGAGAAG        TGAGAAG	CAAGCTCA	ATTTCCAL	TCAGGGTC	TOPEGGETO	CTTCCC	AGTTCACC	CCIGGGG	TCCTGCAC	HILLIIII	TCTCATG	ACTTTCC	CTCTCTCTCT	AAGACTC		ATGGACAC	ATGGACAC	CCAACATO	AATACTTI		CAAATIGGG
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	CCCTTCT	AGGGCGG	HIIIIII	GAGAGTG	HILLILL HILLILL ACCTGCTO	CCAGGAA	TIGIGCC	Tegegee	TEGGGGGG	GCCCACT	TGTCTGT	CTGTGTC	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		ACAGCTAC TGAGCTG!	ACAGCTAC	CCGTCTC			GT-GACA
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Horrigan, S., Soppet, D.R. and Weaver, Z.
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Homo sapiens (human)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata;

Craniata; Vertebrata; Euteleostomi;

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Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford
Tel: 4157259687
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Email: myers@shgc.stanford.edu
Primer A: AGAGACACGGTCAGCCCAAT
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STS size: 188
PCR Profile:
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Polymerization:
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/clone_lib="Human"
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/mol_type="genomic DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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OS Homo sapiens (human)
PN JP 2002507387-A/94
PD 12-MAR-2002
PF 22-DEC-1998 JP 2000526543
PR 24-DEC-1997 US 08/998253,24-DEC-1997 US 08/998255 PR
17-JUL-1998 US 09/118524 PI STEVE
G REED,JIANCCHUN XU
PC C12N15/09,A61K38/00,A61K39/00,A61K39/39,A61K39/395,A61P35/00,
PC C07K14/47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 738 bp
Compounds for immunotherapy and
methods for their use.
Bpl39877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; 1 (bases: 1 to 738) Reed, S.G. and Xu, J. Compounds for immunotherapy and diagnosis methods for their use Patent: JP 2002507387-A 94 12-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C07K16/18, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/53,
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                        Similarity
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                    ACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACA 1769
                                                           GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC
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     ACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACA
                                                                                                                                                                                                                                                                                                                                                                                                         breast cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2071
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                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
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179 c 226 g 17
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100.0%; P
(tive 0;
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1. .738
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of breast
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Homo sapiens kallikrein 5 splice variant 1
cds; alternatively spliced.
AY279380
                                                                                                                                                                                                                                                                                                                                Submitted (19-APR-2003) Pathology and Laboratory Medicine, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                        and Diamandis, E.P.
                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1370)
Kurlender, L., Yousef, G.M.,
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and Diamandis,E.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1370)
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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/codon_start=1
/product="Kallikrein 5 splice variant 1"
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/db_xref="GI:31075481"
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GSNQDLGAGAGEDARSDDSSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQW
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                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                128. .1009
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                              /note="serine
                                                                                                                             /gene="KLK5"
                                                                                                                                                            /gene="KLK5"
                                                                                                                                                                                                    /map="19q13.4"
L. .1370
                                                                                                                                                                                    gene="KLK5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo
                                                                                           ; hK5; alternatively spliced; of GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
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gene 5

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KEYWORDS
SOURCE
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ACCESSION
VERSION
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BD107879
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Best Local (
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36 human secreted proteins.
BD107879
                                                       Ruben,S.M., Soppet,D.R., Ebner,R.,
Brewer,L.A., Olsen,H.S., Duan,R.D.
36 human secreted proteins
Patent: JP 2002500035-A 50 08-JAN-2
HUMAN GENOME SCIENCES INC
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1381)
Homo sapiens (human)
                                                                                                                                                                                                              JP 2002500035-A/50.
                                                                                                                                                                                                                               BD107879.1. GI:23202697
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Conservative (
                          Homo sapiens (human)
JP 2002500035-A/50
06-JAN-1999 JP 2000527554
               08-JAN-2002
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1319. .1324
/gene="KLK5"
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RRIRPTKDVRPINVSSHCPSAGTKCLVSGWGTTKSPQVHFPKVLQCLNISVLSQKRCE
DAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCNGSLQGLVSWGDYPCARPNRPGVYT
NLCKFTKWIQETIQANS"
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ACCESSION VERSION KEYWORDS

AF168768 AF168768.2 Homo sapiens AF168768

GI:20153423

stratum corneum

tryptic enzyme

(SCTE)

mRNA,

complete

PRI 16-APR-2002

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RESULT 13 AF168768 LOCUS

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/mol_type="genomic DNA"
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Umea SE-901 85, Sweden
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Umea SE-901 85, Sweden
3 (bases 1 to 1387)
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Direct Submission
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J. Biol. Chem. 274 (42), 30033-30040 (1999)
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Purification, molecular cloning, and expression of corneum trypsin-like serine protease with possible
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6, 2002 this sequence version
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SKODGAGAGEDARSDDSSSRLINGSDCDMHTQPMQAALLLRPRQLYCGAVUVHPQW
LLTAAHCRKKVERVRLGHYSLSPVYESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKL
RRIRPTKDVRPINVSSHCPSACTKCLVSGWGTTXSPQVHFPKVLQCLNISVLSQKRCE
DAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCNGSLQGLVSWGDYPCARPNRPGVYT
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437 c 351 g
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/note="SCTE; trypsin-like
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170. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/protein_id="AAF03101.1"
/db_xref="GI:6063033"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Diamandis, E.P.
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and Diamandis,E.P.
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                                    /note="serine protease; differentially expressed in malignancy; may play a role in desquamation of skin; hK5; alternatively spliced; similar to the product of GenBank accession Number AF135028"
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PD 08-JAN-2002
PD 08-JAN-1999 JP 2000527554
PF 06-JAN-1998 US 60/070657,07-JAN-1998 US 60/070704 PI
OR-JAN-1998 US 60/070692,07-JAN-1998 US 60/070704 PI
MRUBEN,DANIEL R SOPPET,REINHARD EBNER,DAVID W LAFLEUR, PI
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Ruben, S.M., Soppet, D.R., Ebner, R., Lafleur, D.W., Ni, Brewer, L.A., Olsen, H.S., Duan, R.D. and Rosen, C.A.
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELEPHONE: 415-576-0300
TELEPHONE: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
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not relevant
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TRNGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: not 1
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                                                                         August 5, 2003, 05:12:55; Search time 129.698 Seconds
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-724-394A-20
US-08-724-394A-21
US-08-724-394A-21
US-09-718-896-3
US-09-51-896-3
US-09-520-373D-4
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US-08-757-223-7
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US-09-729-995-3
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                                                - nucleic search, using sw model
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Maximum Match 100%
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Maximum DB seq length: 200000000
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APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 58;
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRES
                          US-07-906-871-15
US-09-780-049-18
US-08-451-778A-7
US-08-451-778A-7
US-08-998-208-7
US-09-791-211-10
US-09-791-211-10
US-09-488-856A-10
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US-09-488-856A-10
US-09-345-882-1
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; Sequence 20, Application US/08724394A
; Patent No. 5872337
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kronmal, Gregory and APPLICANT: Lauer, Peter M. APPLICANT: Ruddy, David A. APPLICANT: Thomas. With Applicant.
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                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                  TOWNSEND and CREW LLP
                                   Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1.246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASIPICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERNCE/DOCKET NUMBER: 017957-00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.576-0200
                                                                                           COUNTAL.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMDIUM TYPE: Floppy disk
AMDIUM TYPE: Floppy disk
AMDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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not relevant
                  TOWNSEND and
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Matches 580; Conservative
CORRESPONDENCE ADDRESS
                                                    San Francisco
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                                                      Gaps
              Length 246240;
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Sequences and Antibodies Thereto
31
                                                  0; Mismatches 120;
                Score 444; DB 2;
Pred. No. 3.1e-81;
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Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Tauchy David A.
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Sequences and An
              22.2%;
80.1%;
                                                    580; Conservative
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              Query Match
Best Local S:
Matches 580
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Matches 580; Conservative 0; Mismatches 120; Indels 24; Gaps 4;	335 TATGATCATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3310 TITIATAAAGACITITITITITITITITITITITITITITITITGAGAGGGAGTCTIGCTCTG 3	Ay 395 TGGCCAGGTGGAGTGGCGGATCTCGGCTCATCTCGCAAGCTCCGCGTCTCCGGGT 454	Qy 455 TCACGCCATTCTCCTGCCTCAGCTCCCAAGTAGCTGGGACTACAGGCGCCCCCCCATAC 514	515 GCCCGGCTAATTTTTCTATTTTTAGTAGACGGGGTTTCACCGTTTTAGCCGGGATG	3130	GCCICGATCICCIGACCICGIGATCCGCCCCCCCCCCCCC	635 GGCGTGACCACCGCCCCCCATCATCATCTTGACTATGCTGATGACAAGTAC	TTATAAAGACTTTTTAGATAAAAACAGAAT	QY 695 CTAAAGCCATCAGACTCTACCCTTTAAATATGGGCCAGGCACGCAC	Db 2958 CTATATCTCTAATGTATGTATTAAGGATGAACCCCGGCTGGGCGCAGTGGCTCACA 2903	Qy 755 CCTGTAATTCCAGCACTTTGGGAGGCAGAGGTGGGTGGATCACTTGAGGCCAGGAGTTTG 814	Db 2902 CCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTAGATCACTTGAGGTCAGGTTGAGTCGGTAGGTCAGTCA	aaaaaaaaa	2842	- Pro をここでもごからごかを正こいをここにかるとれていないのかだったというできます。 ************************************		00 00000000000000000000000000000000000		905 TOTAL CONTROLL CONTROL CO	2674	1055 CAGT 	Db 2614 AAAT 2611	DECITE	US-08-724-394A-20	; Sequence ZU, Application US/U8/24394A ; Patent No. 5872237	; GENERAL INFORMATION: ; APPLICANT: Feder, John N.	; APPLICANT: Kronmal, Gregory S. ; APPLICANT: Lauer, Peter M.	APPLICANT: Ruddy, David A.	; APPLICANT: Tsuchihashi, Zenta . APPLICANT: Wolff Romer K	; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el; TITLE OF INVENTION: Sequences and Antibodies Thereto; NUMBER OF SEQUENCES: 31	pu	wo Embarcadero Center, 8th Floor
Db 2842 AGACCAGCCTGCCCAACACGCGCAAAACCTGTCTCTACTAAAAATACA 2795	934		Qy 935 CGAGAGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACACCACCC 994	995 TCCAGCCTGGGCACAGACTCTGTCTCAATAAATAAATAAA	DD 20/4 TCCAGCCTGGGCGACAGGGTGAGACATCTCCAAAAAATAAAAATAAAATAAAATAAA 2615 Qy 1055 CAGT 1058	Db 2614 AAAT 2611	RESULT 3 IIS-08-724-3948-2276	Sequence 22, Application US/08724394A ; Patent NO. 5872234 CENTEDS THEORYSTON	GENERAL INFORMATION: ; APPLICANT: Feder, John N.	; APPLICANT: Kronmal, Gregory S. ; APPLICANT: Lauer, Peter M.	; APPLICANT: Ruddy, David A.	Tsuchthas	2 5	R OF SEQUENCES:	; CORRESPONDENCE ADDRESS: ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP	; STREEF: Two Embarcadero Center, 8th Floor	≈	Ξ3	COMPUTER: Floppy disk COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-FOS/MS-DOS SOFTWARE: Patentin Release #1 0. Varsion #1 30	FILING DATE: 01-0CT-1996	CLASSIFICATION: 536 ; ATTORNEY/AGENT INFORMATION:	; NAME: Fitts, Renee A. ; REGISTRATION NUMBER: 35,136	; REFERENCE/DOCKET NUMBER: 017957-000100 : TELECOMMINICATION INFORMATION.	; TELEPHONE 115-0200 mm mm mm m m m m m m m m m m m m m	information for SEQ ID NO: 22:	SEQUENCE CHARACTERISTICS: ; LENGTH: 246240 base pairs	; TYPE: nucleic acid ; STRANDEDNESS: not relevant	; TOPOLOGY: not relevant ; MOLECULE TYPE: cDNA	; FEATURE: : NAME/KEY: misc feature	; LOCATION: 1246240 ; OTHER INFORMATION: /note= "HLA-H.CONTIG" US-08-724-394A-22	22.28;	Similarity 80.1%; Pred. No. 3.1e-81;

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3123 AGCCGGGCGTAGTGGCGGGCGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGAGAA 3182
                                                                                 941 TCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGC 1000
                                                                                                      183 TGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCCCGCCACTGCACTCCAGC 3242
                                                                                                                                                                343 TCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAG 402
881 AGCCGGGTGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAG 940
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Sequences and Antibodies Thereto
31
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Pred. No. 2.7e-68;
0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , LUCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         017957-000100
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CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFENCE/DOCKET NUMBER: 017957-00010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Tsuchihashi, Zenta
Wolff, Roger K.
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not relevant
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Best Local Similarity 76.6%;
Matches 553; Conservative
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Ruddy, David A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Med
TITLE OF INVENTION: Sed
NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 380.4; DB 2;
Pred. No. 2.7e-68;
0; Mismatches 141;
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i LOGATION: 1..246240
CTHER INFORMATION: /note- "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                017957-000100
                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   CLASSIFICATION: 330
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01795
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: not relevant
not relevant
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76.6%;
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Best Local Similarity 76.6
Matches 553; Conservative
                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
San Francisco
                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: nc
MOLECULE TYPE:
                                        COUNTRY:
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701 CCATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACGGCGTGGCTCATGCCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                583 CTCCTGACCTC - GTGATCCGCCCCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 AGCCACCGCGCCCGGCCATGATCATCTTGTTGACTATGCTGATGTGACAAGTACCTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 246240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTHARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.0%; Score 380.4; DB 2; ilarity 76.6%; Pred. No. 2.7e-68; Conservative 0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                 CURKENT AFFLICATION NAME:

APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/SERT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION UNDHER: 017957-0001C
REERRINGE/DOCKET NUMBER: 017957-0001C
TELEPHONE: 415-576-020
TELEPHONE: 415-576-020
INFORMATION FOR SED ID NO: 22: SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Best Local S:
Matches 553
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2965 TTTTTAT------CTAAAAAGTCTTTATAAAGGCCGGGCGGGGGCGTGCTCACGCCTGTA
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                                                                                                                                                                        AATTTTTTTTTGTATTTTTAGTAGAGGGGGTTTCACCGTTTTTAGCCGGGATGGCCTCGAT
                                                GCTGGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCA
                                                                                                           TTCTCCTGCCTCAGCTCCCAAGTAGCTGGGACTACAGGCGCCCCGCCACTACGCCCGGCT
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APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: TOWNSEND and TOWNSEND and CREW STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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COUNTRY:
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RESULT 7 US-09-851-896-3/C ; Sequence 3, Application US/09851896, ; Patent No. 6410325 ; GENERAL INFORMATION: ; APPLICANT: C. Frank Bennett ; APPLICANT: Susan M. Freler ; APPLICANT: Andrew T. Watt. ; APPLICANT: Andrew T. Watt.	Oy 1041 AACA 1044	
7 1 1 2000 17		
Query Match 18.3%; Score 366.4; DB 4; Length 70000; Best Local Similarity 74.0%; Pred. No. 1.4e-65; Matches 536; Conservative 0; Mismatches 146; Indels 42; Gaps 4; Qy 349 TITITITITITITITITITITICAGAGGGGTCTGGCCCGGGCTGA 408	Length: 84495   Length: BA495   Length: BAA   TYPE: DNA   TYPE: DNA   CRGANISM: Human   FEATURE:   LOCATION: misc_feature   LoCATION: (1)(84495)   COTHER INFORMATION: n = A/T,C or G	·
OY 409 GIGCAGIGGGGGAICTCGGCTCCACIGCAGCTCCGCCTCCCGGGTTCACGCCAITCTCC 468 111111111111111111111111111111111111	Query Match Best Local Similarity 69.9%; Pred. No. 5.5e-65; Matches 545; Conservative 0; Mismatches 209; Indels 26; Gaps 3;	
OY 469 IGCCTCAGCCTCCCAAGTAGCTGGGACTACAGCCCCCCCCC	OY 357 IIITITITITITITITITICAGACGGAGTCTCGCTCTGTCGCCCAGGCTGCAGTGCAG	
QY 529 TITGIAFITITAGIAGACACGGGGTITCACCGTITIAGCCGGGAIGGCCTCGAICTCCTG 588	Qy 417 GCGGGATCTCGGCTCACTGCAAGGTCCGCGTTCACGCCATTCTCCTGCCTCAG 476	
QY 589 ACCTCGTGATCCGCCTCGGCCTCCCCAAQTGCTGGGATTACAGGCGTGAGCCACCG 648	Qy 477 CCTCCCAAGTAGGGACTACAGGCGCCGCCCACTACGGCTAATTTTTGTATT 536	
QY 649 CGCCGGCCATGATCATCTTCTTGACTATGCTG 681	QY 537 TYTAGTAGAGGGGTYTCACCGTTYTAGCCGGGATGGCCTCGACTCCTGACCTCGTG 596	
OY 682 ATGTGACAAGTACCTAAAGCCATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGC 741	Qy 597 ATCCGCCCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACGGCCGGC	
OY 742 ACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAGGCAGGC	OY 657 CATGATCATCTTGACTATGCTGATGAGAAGTACCTAAAGCCAT 704	
Qy 802 GGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAAACTCTGTCTTTACTAAAAAAA 861	QY 705 CAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACGTGGCTCATGCCTGTAATTC 764	

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US/08/367,841A
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
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                                                               37967 TAGCACTTTGGGAGACAGAGGTGGGAGGACTGCTTGAGCCCAAGCATTCGAGATCAGCCT 37908
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                                 CAGCACTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCT
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; OTHER INFORMATION: EXON: 14539-14581; INTRON: 6791-11583; INTRON: 
; OTHER INFORMATION: 11676-14538; CDS: 11584-11675; 14539-14580
05-08-520-373D-4
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0; Mismatches 97; Indels
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Relatent No. 6451763
GENERAL INFORMATION:
APPLICANT: Tombran-Tink, Joyce
APPLICANT: Chader, Gerald J
APPLICANT: Chader, Gerald J
APPLICANT: Chader, Sofia P
APPLICANT: Becerra, Sofia P
APPLICANT: Rodriguez, Ignacio R
TITLE OF INVENTION: RETINAL PIGMENTED EPITHELI
FILE REFERENCE: 2026-4203031
CURRENT APPLICATION NUMBER: US/08/520,373D
CURRENT FILING DATE: 1995-00-25
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1995-01-25
PRIOR FILING DATE: 1994-07-25
PRIOR FILING DATE: 1992-06-04
PRIOR FILING DATE: 1992-06-04
PRIOR FILING DATE: 1992-06-04
PRIOR FILING DATE: 1992-06-04
SPIOR SEQ ID NOS: 34
SOFTWARE: PATENTIN VONS: 34
SOFTWARE: PATENTIN VON. 2. 1
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Best Local Similarity 76.3%;
Matches 528; Conservative
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ORGANISM: HUMAN
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------CCCATGACCCACTTTTTAAAAACCATCA------
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TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
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Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
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14099 TITITITITITITITITIGAGACGGAGTCTCGCTCGTCGCTCCAGGCTGGAGTACGGTGGC 14040
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
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REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Morgan &
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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PCT-US95-07201-43/c
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ZIP: 10154
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APPLICANT:
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CITY: No
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                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: full length genomic OTHER INFORMATION: sequence for PEDF plus flanking sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.1%; Score 362.8; DB 4; Length 22481; 76.3%; Pred. No. 5.9e-65; 1.ve 0; Mismatches 97; Indels 67;
                                                                    NAME: DOROTHY R. AUTH
RECISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
             APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                         TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.19
Best Local Similarity 76.39
Matches 528; Conservative
                                                                                                                                                                                                                                                          Double
                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                           Unknown
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: P1-147
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67; . Gaps
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                                                                                                                                                                                                                          APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 22481;
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18.1%; Score 362.8; DB 5
76.3%; Pred. No. 5.9e-65;
ive 0; Mismatches 97
                                                                                                                                                                                 Sofia
                                                                                                                                                                     Chader, Gerald J.; Becerra, S
Patricia; Schwartz, Joan P.;
Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                  Morgan & Finnegan, L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NOMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NOMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 Sequence 43, Application PC/TUS9507201 GENERAL INFORMATION:
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Gaps

Length 22484; Indels 418

13980

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13775

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719 TAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAG
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                                                                                                         359 TITITITITITITITITGAGAGICICGCTCTGTCGCCCAGGCTGGAGTGCAGTGGC
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APPLICANT: Poduslo, Shirley E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ASSESSING RISK
TITLE OF INVENTION: FACTORS IN ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 362.8; DB 4
Pred. No. 5.9e-65;
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                                                              0; Mismatches
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2200 Ross Avenue, Suite 2200
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STATE: Texas
LIP: 75201-6776
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"OURTER: IBM PC COMPATIBLE
"TEMPORATION TYPE: PLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-757-223-7; Sequence 7, Application US/08757223; Patent No. 6136530
                      18.1%;
76.3%;
                                                                 Conservative
                                            Best Local Similarity
Matches 528; Conserv
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                      Query Match
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                                        TAGTAGAGGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGATCTCCTGACCTCGTGAT
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APPLICANT: No. 6391850thwestern University
APPLICANT: No. 63918501 Bouck
APPLICANT: No. 63918501 Bouck
APPLICANT: Poul Gillis
TITLE OF INVENTION: Methods and Compositions for
FILE REFERENCE: 0290-23U3
CURRENT APPLICATION NUMBER: US/09/875,223
CURRENT APPLICATION NUMBER: US/09/875,223
CURRENT FILING DATE: 2001-06-06
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1997-07-23
FRIOR FILING DATE: 1997-07-23
FRIOR FILING DATE: 1997-07-23
FRIOR PRIOR PRIOR APPLICATION NUMBER: US 08/899, 304
FRIOR FILING DATE: 1997-07-23
FRIOR PRIOR PRIOR
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LOCATION: 1...22484
CTHER INFORMATION: "n" means either a,
US-09-875-223-2
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Patent No. 6391850
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ORGANISM: Homo sapiens
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US-09-875-223-2/c
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                                                                                                                           APPLICANT: BEASLEY, Ellen M. et al
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01213
CURRENT APPLICATION NUMBER: US/09/820,924
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRASLSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                 Score 353.6; DB 4; Length
Pred. No. 5e-63;
0; Mismatches 149; Indels
                                                                             Sequence 3, Application US/09820924
Patent No. 6555351
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ilarity 72.8%;
Conservative
   1792 GTGTGGTGGTGC 1803
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Best Local Similarity
Matches 549; Conserva
                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 39982
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                                                                                                                                                                                                                                                                                                           Length 5375;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,223
                                                                                                                                                                                                                                                                                                        Score 353.6; DB 3;
Pred. No. 3.2e-63;
0; Mismatches 134;
                          FILING DATE: US/08/757,223
FILING DATE: No. 6136530ember 27,
CLASSIFFCATION: 435
                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REFERENCE/DOCKET NUMBER: 4-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214/740-8865
TELEFAX: 214/740-8800
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5375 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                      Query Match 17.7%;
Best Local Similarity 75.3%;
Matches 551; Conservative
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US-08-757-223-7
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Search completed: August
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                                                                                                                                             GENERAL INCORNATION:
APPLICANT: BEASLEY, Ellen et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1192
CURRENT APPLICATION NUMBER: US/09/818,512
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRSELSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 116592
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Pred. No. 7e-61;
0; Mismatches 219;
                                                    31986 ТСТААААААТААТААТААТАААААААААТАААА 32019
                         1024 TCTCAAATAAATAAATAAACAAACGAACAAGCAG 1057
                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(116592)
COTHER INFORMATION: n = A,T,C or G
US-09-818-512-3
                                                                                                                        Sequence 3, Application US/09818512
Patent No. 6537780
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.2%;
Best Local Similarity 65.8%;
Matches 615; Conservative
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                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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  ---AAAA 16263
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                                             870 AAAAAAAATCAGCCGGGTGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTG
16310 GTTTGAGACCAGCCTGGAAAACATGGCAAAACCCTGTCTCTACT
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5, 2003, 12:11:05

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model	August 4, 2003, 21:01:54; Search time 7120.12 Seconds (without alignments) 11491.278 Million cell updates/sec	US-09-936-271B-13_COPY_1_2000 1 2000 1 999cccagagtgaaggcaaggtgcgtcctgcaccacatc 2000	:: IDENTITY_NUC Gapop 10.0 , Gapext 1.0
OM nucleic - nu	Run on:	Title: Perfect score: Sequence:	Scoring table:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

5777422

Total number of hits satisfying chosen parameters:

2888711 seqs, 20454813386 residues

Searched:

Database : GenEmbl:\*

1: 9b\_ba:\*
2: 9b\_htg:\*
3: 9b\_ni:\*
4: 9b\_on:\*
5: 9b\_ov:\*
6: 9b\_pat:\*
7: 9b\_ph:\*
10: 9b\_pt:\*
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13: 9b\_un:\*
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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMS		ALIGNMENTS
ery tch Length D	11570 11570 11570 237000 237346 23739 33739 131233 1318843 171687 1291137 1291137 100208 119555 117102 119555 119555 119555 119555 119555 119555 119566 119566 119566 119368 119368 119368 119308 1193	
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linear PRI 27-JUN-2000	complete cds.						Euteleostomi;	HOMO.	•		racterization,	
	KLK-L2 gene,						Vertebrata;	i; Hominidae			olecular cha	1 requiation
11570 bp DNA	protein 2						Craniata;	Catarrhin			KLK-L2. M	nd hormona
AF135028 11570	Homo sapiens kallikrein-like protein 2 KLK-L2 gene, complete cds.	AF135028	AF135028.1 GI:4589282	•	Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 11570)	Yousef, G.M. and Diamandis, E.P.	The new kallikrein-like gene, KLK-L2. Molecular characterization,	mapping, tissue expression, and hormonal regulation
AF135028 LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	

RESULT 1

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GTAGAGACGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGATCTCCTGACCTCGTGATCC
                                                                                           GCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCATG
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DRYRRQIDDTMRCAGNGARDSCGGPVVCNGSLQGLVSWGDYFCARPNRPGVYT
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                                                                                                Yousef,G.M., Luot.Y. and Diamandis,E.P.
Direct Submission
Submitted (13.MAR-1999) Pathology and Laboratory Medicine, Mount
Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
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                          2 (bases 1 to 11570)
Diamandis, E.P., Yousef, G.M., Luo, L.Y., Magklara, A.
The new human kallikrein gene family: implications carcinogenesis
Trends Endocrinol. Metab. 11 (2), 54-60 (2000)
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100.0%; Pred. No. 0;
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (01-JUL-2002) DOB Joint Genome Institute, 2800 Mitchell
Burne, Walhut Creek, CA 94598, USA
On Jul 1, 2002 this sequence version replaced gi:14971176.
Draft Sequence Produced by DOB Joint Genome Institute
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Catarrhini; Hominidae; Homo.
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Estimated Total Number of Errors is 0.6.
NOTE: Shatter libraries failed to resolve dinucleotide repeat.
Unsure number of repeat copies 64998-65494. Forced join 65015.
Location/Qualifiers
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Homo sapiens chromosome 19 clone CTB-147C22, complete sequence.
AC011483
                                                                                                 AGGCAGGGAAGGGGCTGGCCTGCCTTCCGGAGCCCCTCCCCATTCTCCGGGCCAGGGAG
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                                          TCCAGGCCCCAAGAATAGTGACCCAGAGTTGGTGAGAAGCCAGATCCTTAAGGCTGGGGG
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DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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Finishing Completed at Stanford Human Genome Center
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Mammalia; Eutheria; Primates;
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DOE Joint Genome Institute.
Direct Submission
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COMPLEMENT (JOIN (13552. 13704.14377. 14530,14678. 14917,
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complement (Join (13552. 13704,14377. 14530,14678. 14917,
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ANISIISDTSCDKSYPGRLTNTWVCAGABGRGAESCEGDSGGPLVCGGILQGIVSWGD
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 230000)

Gan,L., Lee,I., Smith,R., Argonza-Barrett,R., Lei,H., McCualg,J., Moss,P., Paeper,B. and Wang,K.
Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region

Gene 257 (1), 119-130 (2000)
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Gan L., Lee, I., Smith, R., Argonza-Barrett, R., Lei, H., McCuaig, J. Moss, P., Paeper, B. and Wang, K.
Direct Submission
Submitted (09-WAR-2000) Chiroscience R & D Inc., 1631 220th St.
Bothell, WA 98021, USA
Location/Qualifiers
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9482. .9641,11472. .>11517))
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/db_xref="taxon:9606"
/chromosome="19"
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9 4 9 4 9 4 9 4 9 4 9 4 9 4 9 4 9 4 9 4	120   GARGAAAGGGAGAGGGAGGGAGGCAGAAAGACAGGGAAGGGAAGGGGAGGGTGGG   14242     120   GAAGAAAGAGAGAGAGAGAGAGAATAACAAACTACAGAAACACAGAGAACA   179     42428   GAAGAAAGAGAGAGAGAGAAATAACAGAACAACTACAGAAACACAGAGAACA   14236     140   141   141   141   141   141   141   141   141   141   141   141   141   141     42368   CACAGAGACCTGGGACACAGGGACACACAGAGCAGAAAAAAAA	42308 GACACAAATGGAGACACAGAGGTGTAAAGAAGAGATTAACAGAGTCCCAGATACAG 14224- 300 CAAAGGGGCAGAAGCACAGTTTTCAGGGTGTGTCTTTATTTTTTTT			CAGAGGTGGGTGATCACTTGAGGCCAGGAGTTTGAGGCCAGCCTGGCCAACTTGTGTAAAAAAAA	GGAGGTTGCAGTGGGCCGAGATCACCCCCCCCCCGGCCGG

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Quality coverage: 10.7 in Q20.

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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States, 1. Collists, 1. Cander, E., Abraham, H., Allen, N., Anderson, S., Barrah, V., Bedaf, F., Boguslavkiy, L., Burkert, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Ferreira, P., FitzHugh, W. Gage, D., Galagan, J., Sardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Heaford, A., Horton, L., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., Moczarthy, M., McEwan, P., McKernan, K., Morrow, J., Murphy, T., Naylor, J., Nurphy, T., Sondore, J., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Santos, R., Voung, G., Zainoun, J., Stojanovic, N., Zimmer, A. and Zody, M., Santos, T., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Santos, T., Young, G., Zainoun, J., Stojanovic, M., Stojanovic, N., Zimmer, A. and Zody, M., Santos, T., Young, G., Zainoun, J., Stojanovic, M., Stojanovic, M., Zimmer, A., and Zody, M., Santos, M., Young, G., Zainoun, J., Stojanovic, M., Stojanovic, M., Stojanovic, M., Stojanovic, M., Stojanovic, M., Stojanovic, M., Salmer, S., Stojanovic, M., Stojanovic, M., Stojanovic, M., Stojanovic, M., Waman, D., Ye, W.J., Young, G., Zainoun, J., Stojanovic, M., Stojanovic, M., Stojanovic, M., Stojanovic, M., Stojanovic, M., Waman, D., Ye, W.J., Young, G., Zainoun, J., Stojanovic, M., Stojanovic,
                                                Sirren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Cooke, D., Deraer, R., Dewar, K., Dawar, K., Diaz, J.S., Collymore, A., Cooke, D., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D. Oodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lancque, K., Landaraer, S., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McGarthy, M., McFwan, P., McGurk, A., McKernan, K., McPheeters, R., McHarin, J., Menneus, L., Mihova, T., Miranda, C., Peterson, K., Peterson, K., Peterson, K., Peterson, K., Peterson, K., Peterson, K., Santcs, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J., Subrission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 15, 2000 this sequence version replaced gi:11136831. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Sequencing vector: Plasmid; n/a; 69% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 2130748 bases at least Q30
Consensus quality: 213655 bases at least Q30
Consensus quality: 215058 bases at least Q20
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Insert size: 216246; sum-of-contigs
Quality coverage: 11.9 in Q20 bases; agarose-fp
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Length 217346;

1107 others

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ACL30782 200792 bp DNA linear HTG 22-NOV-2002 Pan troglodytes clone CH251-355A20, WORKING DRAFT SEQUENCE, 12 ordered places.
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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Abhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,
Laric, P., Lee-Lin, S.-Q., Legaspi, K., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A.,
Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,
Wetherby, K. D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes (chimpanzee)
pan troglodytes
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                     202590 AGTGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCAC
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202710 TAGGGGGGGGGGGGGGGGGGTATTGCTAAGGCCCGATAGGCACCTCATTGCCCGGGAATGT
                                                                                                           AGTGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGGAGCAAATCCCCCAC
                              1730 TAGGGGGAGCAGGAGGTATTGCTAAGGCCCGATAGGCACCTCATTGCCCGGGAATGT
                                                                                           The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Green.E.D.

Direct Submission
Submitted (14.AdG-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 200792)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: NIH Intramural Sequencing Center
Center code: NISC
                                                                                                                                                                                                                                                                                               202470 GAGAGGTGTCTGTGCGTCCTGCACCCACATC 202440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------- Project Information
                                                                                                                                                                                                                                                                               1970 GAGAGGTGTCTGTGCGTCCTGCACCATC 2000
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Center clone name: 355A20
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 28306: contig of 28306 bp in length 28407 37856: contig of 9450 bp in length 37957 37956: gap of unknown length 73522: contig of 9456 bp in length 73522: contig of 945 bp in length 73523 73522: contig of 945 bp in length 83568 88867: contig of 5150 bp in length 83568 88867: contig of 5150 bp in length 83568 88817: contig of 5150 bp in length 83568 88817: contig of 5150 bp in length 83688 88817: contig of 5150 bp in length 88818 88818 88817: gap of unknown length 88918 88917: gap of unknown length 88918 88917: gap of unknown length 88918 88917: gap of unknown length
clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least BX average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                           Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 196656 bases at least Q40
Consensus quality: 197883 bases at least Q20
Insert size: 215000; agarose-fp
Insert size: 215000; agarose-fp
Unsert size: 199692; sum-of-contigs
Quality coverage: 9.03x in Q20 bases; sum-of-contigs
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unknown length
of 34168 bp in length
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186482: gap of unknown length
193344: contig of 6862 bp in length
193444: gap of unknown length
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200792: contig of 1329 bp in length
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                                                                                                                                                                                                                                                                                                                                654 GGCCATGATCATCTTGACTATGCTGATGTGACAAGTACCTAAAGCCATCAGACTCTA
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                                                                                                                                                                                                                                                             61.4%; Score 1227.2; DB 2; Length 200792; 95.5%; Pred. No. 3.4e-292; 1ve 0; Mismatches 18; Indels 45; G
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/note="assembly_fragment"
159980. .174698
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phasmid; n/a; 100% of reads Assembly program: Phasmid; n/a; 100% of reads Consensus quality: 171127 bases at least Q40 consensus quality: 17124 bases at least Q20 lesert size: 188000; agarose-fp contigs (autity coverage: 8.76x in Q20 bases; sum-of-contigs Quality coverage: 8.76x in Q20 bases; sum-of-contigs
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* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 6527 6626; contig of 61286 bp in length 6527 6626; gap of unknown length 6527 6626; contig of 12186 bp in length 18913 18912; gap of unknown length 61801 97068; contig of 83108 bp in length 61801 97068; contig of 28038 bp in length 61801 97068; contig of 28038 bp in length 77089 97168; gap of unknown length 77089 125206; contig of 28038 bp in length 77089 125206; contig of 28038 bp in length 77089 125206; contig of 28038 bp in length 77089 125206; contig of 1715 bp in length 77081 125307 127021; gap of unknown length 77089 17081; gap of unknown length 77081; gap of unknown length 77089 17081; gap of unknown length 77081; gap of unknown length 7708
Submitted (08-AUG-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 176647)
                                                                                                                              Sequencing Center, 8717, USA
                                                                                                                           Submitted (14-NOV-2002) NIH Intramural Sequencing Center, 8 Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 14, 2002 this sequence version replaced gi:22138439.
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of 6365 bp in length.
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                                                                                                                                                                                                                                                             Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
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                                                                                                         Direct Submission
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                                                                                Green, E.D.
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E 1 (bases 1 to 17647)

S Akhter, N. Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Boutfard, G.G., Brinkley, C., Brooks, S.,
Carlaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,
Laric, P., Lee-Lin, S.-G., Legaspi, R., Maduro, O.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,
Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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HTG; HTGS_PHASE2; HTGS_DRAFT.
Papio anubis (olive baboon)
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QY         1076 TATCT AAAAAAAAAAACCTGTCAACAAATAGAGCAGAAGTGAAATAAAGGAAAATAA 1132           DD         1101	1193 ATCACAGAGCATAGAAAGACAGGGAGGAACAGGAGAACACCTGTGGCCC	1309   AGACAGACAGAAAAAGACAGAGAGAGAGAGAGAGAGAGA	AAGATAGCCGAGGGAGAACCAGAGAGATGGAAGACTCTG	0.0   0.0	1769 CACCTCATTGCCCGGGAATGTGCCCCAGGGGCGGTGGTTATAACTCAGGCCCGGT 1828	1949 GTGGCTCAGCAGGAAGGAGAGGTGTTGTGCGTCCTGCACCCACATC 2000   1949 GTGGCTCAGCAGGGAAGGAGGTGTTGTGCGTCCTGCACCCACATC 2000   1111  1  1  1  1  1  1  1  1  1  1  1
	1652 /note=" clone_e vector_ 6627 . /note=" /note="	misc_feature 61881. 97068  misc_feature /note="assembly_fragment"  misc_feature /note="assembly_fragment"  misc_feature 116911. 176647  misc_feature /note="clone overlaps with GenBank Accession Number Accession		Gaps TACCCT 71	1410 ATCATCCTCTTGATTATGGTGTGTGACAGGTACCTAAAGCCATCAGACTCCACCCT 1351 718 TTAAATATGCTGTTGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGA 777 1111111111111111111111111111111111	1230   AAACCCCATCTTTTTTTTTTTTTTTTTTTTTTTTTTT

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note="single stranded/single chemistry region"
8265. .9528
note="single stranded/single chemistry region"
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5432. .5518
/note="single stranded/single chemistry region"
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note="single stranded/single chemistry region"
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replace=""
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'note="delted in clone: XX-540F24"
'replace=""
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note="deleted in clone: XX-540F24"
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hote="deleted in clone: XX-1Bcos"
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.266. .5317
note-"low quality region"
.266. .5317
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note="low quality region"
1766. :11880
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                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 32799)
                                                                                                                                                                                                                                                                                     Submitted (26-NOV-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany 1 (bases 1 to 37799)

Lagemann, D. and Platzer, M.

Submitted (05-DEC-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany Center: Institute of Molecular Biotechnology

Center: Institute of Molecular Biotechnology
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All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                               Submitted (07-MAX-1997) Genome Analysis, Institute Of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany (bases 1 to 32799)
Lagemann, D. and Platzer, M.
Direct Submission
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Sequencing vector: PUCL38; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 32776 bases at least Q40
Consensus quality: 32770 bases at least Q30
Consensus quality: 32770 bases at least Q30
Consensus quality: 32770 bases at least Q30
Quality coverage:13.12x
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note-"single stranded/single chemistry region"
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note="single stranded/single chemistry region"
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/note="single stranded/single chemistry region"
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'note="single stranded/single chemistry region"
                                                                                                                      Rump, A., Rosenthal, A., Drescher, B. and Schattevoy, R. Direct Submission
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/note="single clone coverage"
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note="low quality region"
166. .3173
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
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/clone="XX-B6cos"
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variation 15481. 15483  variation //note=-/abstrad in clone: xx-540P24*  variation //note=-/abstrad in clone: xx-540P24*  variation //note=-/abstrituted in clone: xx-540P24*  variation //note		805 CAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACTCTGTCTTTACTAAAAAAAA	985   ATCACCGCCTCCAGCCTGGGCGACAGACTCTGTCTCAATAAATA	5540 AGGAGAAGAAGGAAGGAAGGAAGAAGAAAGAAAGAAGAA	OY 1463 GACTCTGAGAAAAAACAGAGAAAAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS95C20 138849 bp DNA linear PRI 05-MAR-2003
Human DNA sequence from clone RPI-95C20 on chromosome Xpl1.3-11.4,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Web site: http://www.sanger.ac.uk
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297181.1 GI:3059064
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Direct Submission
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Consensus quality: 139579 bases at least Q40
Consensus quality: 140059 bases at least Q30
Consensus quality: 140059 bases at least Q30
Consensus quality: 140054 bases at least Q30
Consensus quality: 140054 bases at least Q30
Estimated insert size: 140000; agarose-fp estimation
Batimated insert size: 140000; agarose-fp estimation
Quality coverage: 8.77 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "Working draft' sequence. It currently
* Consists of 3 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the flished sequence
* as soon as it is available and the accession number will
* be preserved.
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Submitted (09-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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1197: gap of unknown length
18670: contig of 1743 bp in length
18770: gap of unknown length
141923: contig of 123153 bp in length.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
Homo sapiens (human)
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Pred. No. 5.6e-102;
0; Mismatches 139;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Center: Joint Genome Institute
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        regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sww; SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping group. Further information can be found at
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                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chrx
RRD-95C20 is from the library RRCI-1 constructed by the group
Pieter de Jong, For further details see
http://www.chori.org/bacpac/home.htm
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44152 a 27174 c 27490 g 40033 t
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="RP1-95C20"
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les 583; Conservative
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PRI 01-JUN-2002
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1 (bases 1 to 171697)
1 (bases 1 to 171697)
1 (kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
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Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 To bases I to 171697)

Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.

Direct Submission
Submitted (12-MAR-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases I to 171697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 1, 2002 this sequence version replaced gi:19352302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 3 clone RP11-728B21, complete sequence. AC114876.2 GI:21306686
                                                                                                                       CTGAGGCACGAGAGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACAT
AAAAAAAAAAAATCAGCCGGGTGTCGTGGGGCACACCTGTAATCCCCAGCTATGCTGGAGG
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Sequencing vector: plasmid; 47% of reads
Sequencing vector: plasmid; L08752; 0% of reads
Sequencing vector: plasmid; L08752; 0% of reads
Chemistry: Dye-terminator E1; 89% of reads
Chemistry: Dye-terminator Big Dye; 11% of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 171547 bases at least 0,00
Consenus quality: 171691 bases at least 0,00
Consenus quality: 171697 bases at least 0,00
Insert size: 171697; sum-of-contigs
Quality coverage: 9.2x in 0,20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: University of Washington Genome Center
Center: University of Washington Genome Center
Center Code: UWG
Web site: http://www.genome.washington.edu
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5': RP11-349E16 (UWGC:bc0646) AC098481
3': RP11-624D20 (UWGC:bc0494) AC068222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project Information
Center project name: chr-3
Center clone name: RP11-728B21 (bc0540)
                                                                                                                                                                                                                                                                                                                                                                                                       1047 CGAACAAGCAGTTTGTTGTACCTTAGTTATA 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Unpublished
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9092	4641	1708	6082	1904	4433	1799	23885	; ; ; ; ;																				
4508 1054 3396 1054	3122	<800	4687	<800	5041	1314	3122	7057	1054	2421	1646	2867	6048	6386	<800	3396	3950	2029	3630	3229	0 0		0087		0000	1314	<800	<800
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oe quality program. sed to quality zero. have less than ally visible from the	ss otherwise noted: sequenced with an lity data (i.e., Phred	iolve all sequencing ; all regions were promore than one M13	y restriction digest.	ple Complete Digest	Nentally derived digest Its is given below. Sists of both insert and	the entire circular BAC. approximately 400-800 bp)	nence do not appear	nues. Uniquely ordered	ECO FINAL PROPERTY OF THE PROP	Sequermap Engrernt	9698	0.08>	3464	334 <800			3694 3709	Ł.	13221 13066	8640 8687	5654 5681	2842 2844	10800 10593	11874 11745	8529 8687	286 <800	6660 6724	13999 13754
tth°sequence quality assembly program. seen reduced to quality zero. setted to have less than not generally visible from the a available as part	llows unless otherwise noted: rranded or sequenced with an / high quality data (i.e., Phred	ade to resolve all sequencing ind repeats; all regions were	onfirmed by restriction digest.	by Multiple Complete Digest	ne experimentally derived digest ed fragments is given below.	represent the entire circular BAC. cutoff (approximately 400-800 bp)	tint and hence do not appear	editions.	ECO		9698	9			951	4919		555			₹!	2 :		4.				<u>و</u> ،
annotated with sequence quality by the Phrap assembly program. bases have been reduced to quality zero. e 40 are expected to have less than p. q. values are not generally visible from the ormat but are available as part	nished as follows unless otherwise noted: her double-stranded or sequenced with an or covered by high quality data (i.e., Phred	ttempt was made to resolve all sequencing mpressions and repeats. all regions were namen alsemid subclone or more than one M13	sembly was confirmed by restriction digest.	een validated by Multiple Complete Digest	parison of the experimentally derived digest ence-predicted fragments is given below. Ingested sequence consists of both insert and	accurately represent the entire circular BAC.	the ingerprint and hence do not appear are no significant remaining discrepancies	encal and predicted values. Uniquely ordered ated by dashed lines.	ECOLUMN CONTRACTOR	SequerMap	9698 6790 8696	9	3403	334	7924 951	10372 4919	3694	2867 555	13221	8640	5654	2842	10800	11874	8529	286	0999	13999
requence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred	34); an attempt was made to resolve all sequencing uch as compressions and repeats; all regions were at least one plasmid subclone or more than one M13	nd the assembly was confirmed by restriction digest.	Sequence Validation: This sequence has been validated by Multiple Complete Digest	fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and	order to accurately represent the entire circular BAC. Iments below a variable cutoff (approximately 400-800 bp)	ssolved in the ingerprint and hence do not appear	Derween ine experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.	HINGILI ECO	rngrPrnt Sequermap	9698 6790 8696	6382 6450	<800 3403	<800 334	7940 7924 951	10618 10372 4919	<800 3694 	2795 2867 555	1521 13221	9389 8640	3015 5654	10372 2842	883 10800	1054 11874	1314 8529	883 286	4687 6660	7564 13999

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This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered
                                                                                                                                                                                       Rouse, G., Wu, Z.,
Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality -= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                  and Haugen, E.D.
Direct Submission
Submitted (15-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 15, 2002 this sequence version replaced gi:16328287.
                                                                                                                    Submitted (23-OCT-2001) Genome Center, University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; L08752; 100% of read Chemistry: Dye-terminator ET; 76% of reads Chemistry: Dye-terminator B1; 76% of reads Assembly program: Phrap; version 0,990319 Consensus quality: 227162 bases at least Q40 Consensus quality: 227131 bases at least Q30 Consensus quality: 227137 bases at least Q30 Insert size: 227137; sum-of contigs
                                                                                                                                                                                                                                                                                                                                                         Center: University of Washington Genome Center
                                                                     Olson, M.V., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
                                                                                                                                      Box 352145, Seattle, WA 98195, USA
3 (Dases 1 to 227137)
Kaul, R. K. Olson, M. V. Zhou, Y. James, R.A.,
Saenphimmachak, C., Phelps, K.A., Buckley, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project Information
Center project name: chr-3
Center clone name: RP11-349E16 (bc0646)
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                                               (bases 1 to 227137)
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                                                                   Kaul, R.K., Olson, P
Direct Submission
                                                                   AUTHORS
TITLE
JOURNAL
                      JOURNAL
REFERENCE
                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                    REFERENCE
                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                   COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 227137)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
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                                                                        Gaps
                                                                        13;
                      Length 171697;
                                                                   Indels
                                               Pred. No. 1.4e-101;
0; Mismatches 140;
                      DB 9; L
1.4e-101;
                      Score 455;
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                   22.8%;
78.9%;
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61 <800 44 <800 7321 7358	1877 2371 2346 2226 22	453 1416 6367 6431	4145 3577 3633 5827	1772 17419 303 <800 371 <800	629 <800 5615	3003 2820 2850 7814		3887 1553 1517 978	74 <800 1792 .1741 2723 2775	0 2088 7744 7870	73 <800 18454 18910 2540 2595	5809 4671 4671 4019	1186 8958 9045 3118	5 4376 5282	6405	1719 1681 5052	<800 432	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Query Match 22.8%; Score 455; DB 9; Length 227137; Best Local Similarity 78.9%; Pred. No. 1.5e-101; Matches 572; Conservative 0; Mismatches 140; Indels 13; Gaps 2;	Qy 326 GGTGGTGTGTGATCATCTTTTTTTTTTTTTTTTTTTTTT	DD 91443 GATGGTTCATTTCTCTCAGGTTTTTTTTTTTTTTTTTTT	Qy 386 CTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGGATCTCGGCTCACTGCAAGCTCCGC 445	446 CTCCCGGGTTCACGCCATTCTCCTGCCTCAGCTCCCCAAGTAGCTGGGACTACAGGCGCC 505	Db 91563 CTCCCAGGTTCACGCCATTCTCCTGCCTCAGCCTCCGAGTAGCTGGAGCTACAGGCGCC 91622	Qy 506 CGCCACTACGCCCGGCTAATTTTTTTTTAGTAGAGGCGGTTTCACCGTTTTA 565	Db 91623 CGCCACCACGCCGGCTAATTTTTTTTTTTTTTAGTAGACGCGGTTTCACCGTGTTA 91682	GCCGGGATGGCCTCGATCTCCTGACCTCGTGATCCGCCCCCCCTCGGCCTCCCAAAGTGCT 625	Db 91683 GCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGC	Qy 626 GGGATTACAGGCGTGAGCCACCGGCCCGGCCATGATCTTCTTGACTATGCTGATGT 685	686 GACAAGTACCTAAAGCCATCAGCCTTTAAATATGCAGTTTGGCCACCG	91802
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4 (bases 1 to 119147)
Waterston, R. H.
                                                                                                                                                                                                                                                                                            USA
                                                                                                                                             AAAAAAAAAAAATCAGCCGGGTGTCGTGGGGCACCTGTAATCCCAGCTATGCTGGAG 925
 GCTGAGGCACGAGAGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACA 985
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                                                                                                        91922 CGGAGTTCGAGACCAGTCTGGCCAACGTGTCAAAACCCCATCTCTACT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens BAC clone RP11-793H20 from 4, complete sequence. AC098873 AC036224 G1:18855169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases,1 to 119147)
Waligorski,J., Haakenson,W. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-793H20
Unpublished (2001)
3 (bases 1 to 119147)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sapiens@watson.wustl.edu
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Sulston, J.E. and Waterston, R.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                    between neighboring data submissions.
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0.0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by otherwise noted: This sequence was finished as follows unless restriction digest.

## MAPPING INFORMATION:

Louis Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Cataneso, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-260K18, 2000 bp overlap; the clone sequenced to the right is RP11-473M2. Actual start of this clone is at base position 106515 of RP11-260K18; actual end is at base position 119147 of RP11-793H20.

Single plasmid region exists between 77265 and 77307. Polymorphisms exist between AC079118, AC024191 and AC098873.

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The sequence of AC036224 has been incorporated into AC098873
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2959. .3655
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30890 CTAAAATTTCCATATTTCCCTCAGATGGAAAAATGATAACACCAGTAGAAGTTTTAATAG 30949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                791 GAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACTCTGTTTT
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                Length 119147;
                                                                                                                                                                                                                                                          21;
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(NID:9828631)"
26136. .26251
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                              Score 452.4; DB 9;
'' Pred. No. 6e-101;
'0; Mismatches 126;
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1larity 80.0% Pred. No. 6e-
Conservative 0; Mismatches
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26252. .26537
/rpt_family="Alu"
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18576. 18866
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11350. .22285
note="CpG_island (%GC=69.3, o/e=0.90, #CpGs=92)'
1695. .21995
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9143. 9317
/rpt_family-"MER1_type"
9465. 9696
/rpt_family-"MIR"
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23993. .24105
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628. .8786
rpt_family="MER1_type"
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1005. .11078
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/rpt_family="ERVK"
23247. ??**
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22445. .22671
/rpt_family="MIR"
22674. .22791
22792. .23246
                                                                                 /rpt_family="MIR"
8013. .8086
/rpt_family="L2"
8306. .8622
                                       rpt_family-"MaLR"
581. .7819
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16646. 16022
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0553. .10574
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5788. .15946
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286. .11384
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'520. .17816
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31117

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complement(2472. .2666)
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                                                                 COMMENT
                                                                               Direct Submission
Submitted (23-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Worley.K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 108893)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 108893)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Dases 1 to 108893)
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108893)
AC079169.32 GI:21263154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1 to 108893)
                          sapiens (human)
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             KEYWORDS
VERSION
                         SOURCE
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SEQUENCING READ COVERACE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Iow Coverage.
                                                                                                                                                                                                                                                                                                                                            CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
Worley, K.C.

Direct Submission

Submitted (22-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Om May 30, 2002 this sequence version replaced gi:21206031.

INFORMATION: http://www.hgsc.bcm.tmc.edu/oremail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

    2067
    note="overlaps bases 108750. 110816 of clone AC002404"

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/rpt_family="Alusx"
complement(1760...2236)
/rpt_family="LiM4b"
2259...2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="clone overlap"
complement(549. .580)
/rpt_family="LlM4"
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1. .108893
/organism="Homo sapiens"
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/rpt_family="Alusx"
complement (872. 1369)
/rpt_family="LiM4"
1370. 1394
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANNOTATION OF FEATURES:
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1084 1065 1752 77 <800 1057 76 776 297 619 <800 10235 1	<pre></pre>		2655 6031 2655 2688 2655 2688 213 <800 213 <800 432 <800 688 <800 172 <800 172 <800 172 <800 172 <800 172 <800 173 <800 174 S
	4008 46 1990 11 1990 11 5242 55 846 846 846 823 823 823 823 823 823 823 823		FEATURES Location source 1.100
Drafting Center: SC	onsensus quality: 100206 bases at least 040 onsensus quality: 100207 bases at least 030 onsensus quality: 100208 bases at least 030 nesert size: 100208; sum-of-contigs uality coverage: 25.1x in 020 bases; sum-of-contigapting Sequences:  ***RP11-297123 (UWGC:sc0384) AC098656, 3777-bp ov.: RP5-871E2 AL161797, 3773-bp overlap nec Quality Assessment:  ***entry has been annotated with sequence quality mates computed by the Phrap assembly program.  manually edited bases have been reduced to quality mates computed by the expected to have less that ity levels above 40 are expected to have less that for in 10,000 bp.  -by-base quality values are not generally visible ank flat file format but are available as part	all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mis subclone; and the assembly was confirmed by restriction digest.  Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.  HindIII B9111	SeqDerMap         Fight         SeqDerMap         Fight         SeqDerMap         Fight         4462           27861         27870         2775         2822         4460         4442           10835         10615         15690         15691         2067         2066           8         <800

Rouse, G., Wu, Z., Kibukawa, M., Raymond, C.

and

Raymond, C., Clendenning, J., Ivey, R.G.

Rouse, G., Wu, Z., Kibukawa, M., Raymond, C.

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Center, University USA

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182569)
                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (31-MAY-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On May 31, 2002 this sequence version replaced g1:14702054.
Center: University of Washington Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RP11-107013 (UWGC:bc0229) AC099539, 25534-bp overlap RP5-1053D16 (UWGC:bc0709) AC006515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13: L08821; 46% of reads Sequencing vector: plasmid; L08752; 54% of reads Sequencing vector: plasmid; L08752; 54% of reads Chemistry: Dye-terminator ET; 36% of reads Chemistry: Dye-terminator ET; 36% of reads Chemistry: Dye-terminator B19 Dye; 59% of reads Chemistry: Dye-terminator B19 Dye; 59% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 182265 bases at least Q40 Consensus quality: 182511 bases at least Q30 Consensus quality: 182519 bases at least Q30 Consensus quality: 182559 bases at least Q20 Insert size: 182569; sum-of-contigs Quality coverage: 7.6x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
                                                                                                                                                                                                                                                                                             Kaul, R., Olson, M.V., Zhou, Y., James, R.A., Saenphimmachak, C., Phelps, K.A., Buckley, D.,
                                                                                 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Saenphimmachak, C., Phelps, K.A., Buckley, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: chr-3
Center clone name: RP11-111P21 (bc0233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Project Information
                                                                                                                                                                                                                                            Submitted (12-JUL-2001) Genome
Box 352145, Seattle, WA 98195,
3 (bases 1 to 182569)
                                                                                                                                                                     2 (bases 1 to 182569)
Kaul, R.K., Olson, M.V.,
Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Overlapping Sequences:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center Code: UWGC
 Homo sapiens (human)
                                                                                                                                          Direct Submission
                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                    and Haugen, E.D.
                                                                                                                                                            Unpublished
SOURCE
ORGANISM
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REFERENCE
AUTHORS
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                                                                                                                                                                                             39;
                                                                                                                                                          Length 100208;
                                                                                                                                                                                             Indels
                                                                                   /clone_lib-"RPCI human BAC library 11"
20265 c 19464 g 29311 t
                                                                                                                                                          Score 450; DB 9; 1
Pred. No. 2.3e-100;
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0; Mismatches
              /mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-298P9"
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This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and
                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                           problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Validation:
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182569 bp DNA linear PRI 31-MAY.
Homo sapiens chromosome 3 clone RP11-111P21, complete sequence.
AC092500 AC063916
AC092500.2 GI:21281542
HTG.

DEFINITION ACCESSION VERSION KEYWORDS

LOCUS

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37323 GGTGGTGGGCACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAAGGCCGTGAAC 37382
                                                                                  891 CGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGGGGCACGAGAGTCACTTGAAC 950
                                                                                                                       1011 GAGCAAGACTCTGTCTCAAATAAATAAATAAACAAACGAACA 1052
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Search completed: August 5, 2003, 09:57:01 Job time: 7130.12 secs

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10934.739 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                    1 gggcccagagtgaaggcaag......gtgcgtcctgcacccacatc 2000
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| SIDSI/gcgdata/geneseq/geneseqnembl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqnembl/NA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqnembl/NA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqnembl/NA1984.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
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## ALIGNMENTS

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Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
kallikrein-like protein; serine protease; cytostatic; cancer;
prostrate cancer; ds.
         AAA95905 standard; DNA; 11570 BP.
                                                                                                                                                                                                                         (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                               99US-0127386.
99US-0144919.
                                                                                                                                                                     09-MAR-2000; 2000WO-CA00258
                                                                                                                                                                                       99US-0124260
                                            02-FEB-2001 (first entry)
                                                                                                                                                                                                                                           Yousef GM, Diamandis EP;
                                                             Human KLK-L2 gene.
                                                                                                                                  WO200053776-A2.
                                                                                                                 Homo sapiens
                                                                                                                                                                                               01-APR-1999;
21-JUL-1999;
                                                                                                                                                                                       11-MAR-1999;
                                                                                                                                                   14-SEP-2000
                          AAA95905;
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WPI; 2000-587440/55

900 900 960 960 1020

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AATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAGGC
                       AATATGCAGTTTGGGCCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAGGC
                                              AGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAA
                                                        GAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCCTGGGCGACAGAGCAAGACT
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                        KLK-L
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                      New kallikrein-like (KLK-L) proteins for
protein mediated disorders, especially ca
                                                       Claim 1; Page 143-149; 184pp; English.
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The present genomic sequence is that of human pituitary adenylate cyclase estivating polypeptide (PACAP). This gene is localised to the short arm of chromosome 18p11 and synthesised in the retinal ganglion cells. The genomic DNA is isolated from lymphocytes of individuals. The coding
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AGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCCACCCCTGG
                                                                                   a dinucleotide repeat polymorphism an STS marker, ADCYAP1"
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for diagnosis of bi-polar
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affective disorder and schizoaffective disorder manic type
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marker, W3440 and
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region of the gene has a dinucleotide repeat polymorphism marker known as W3440 and an STS marker, ADCYAP1 is located in the 3'UTR. These markers are useful to map the gene physically and genetically to the chromosome 18. This sequence can be used to design probes for detecting the presence or absence of a mutation in the wild type PACAP gene. It is also useful for genetic diagnosis of neuropsychiatric disorders like bipolar affective disorder lepton polar affective disorder like bicalinical observation and subjective reports. It is used for identifying compounds that modulate PACAP gene expression which are useful for
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                                                                                                                                                                                    Score 424.4; DB 20; Length
Pred. No. 1.4e-65;
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0; Mismatches 146;
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Best Local Similarity 75.4%;
Matches 617; Conservative
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                                               drug toxicity
                       Homo sapiens.
       14-AUG-2002
                            11-APR-2002
    ABK83562;
 ABK83562/c
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parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
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Also included are modulating (M2) GA by contacting of with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the corront of in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the choice of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation of gene(s) from GS in the tissue. MI is useful for detecting GCA, M2 is useful for modulating GA, M3 is useful for screening an inflammation in a tissue; M4 is useful for expectably in an inflammation in a tissue, an allergic response in a subject to a pathogen or sterile correcting an inflammation (especially chronic) in a tissue, and a tissue, an allergic response in a subject to a pathogen or sterile correcting an inflammation (especially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile correcting an inflammation (especially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile correcting an inflammation of a pathogen or sterile correcting an allergic response in a subject to a pathog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                        Human cDNA differentially expressed in granulocytic cells #133.
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                                                                                                                                                  ABK83562 standard; cDNA; 139904 BP
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                                                                                            Gaps
                                              Length 139904;
Sequence 139904 BP; 39268 A; 29759 C; 30173 G; 40704 T; 0 other;
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                                              Score 416.6; DB 24; Length
Pred. No. 3.4e-64;
0; Mismatches 129; Indels
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                                                Query Match 20.8%;
Best Local Similarity 79.1%;
Matches 551; Conservative
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2000US-0233064. 2000US-0233065. 2000US-0234223. 2000US-0234274.

2000US-0233063

14 - SEP - 2000; 21 - SEP - 2000; 21 - SEP - 2000; 2000US-0235834. 2000US-0235836. 2000US-0236327.

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27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 02-OCT-2000;

2000US-0235484

25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 00000S-0237039

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-OCT-2000; -OCT-2000; -OCT-2000;

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-OCT-2000;

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Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirhoulmatic; antiproliferative; cytostatic; cardiant, neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperpoliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; ocular disorder; assistrointestinal disorder; reaplicative; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.
                                                                                                                                                                                                  2000US-0179065.
2000US-0180628.
2000US-0184664.
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2000US-0190076.
2000US-0198123.
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05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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                                                                                                                     Homo sapiens
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08-NOV-2000;

20-OCT-2000 01-NOV-2000

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15449 CACCCGGCC----GATGTTTGCAACTCTTTAACAGTGAAAACAAATCCCAGCTTTTA-- 15501
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                                                                                                                                                                                                    709 CICTACCCTITAAATATGCAGTTTGGGCCCAGGCACCGTGGCTCATGCCTGTAATTCCAGC
                                                                       -----TAAAATATATAAAGCTGGGCTGGCCGGGGCTCACACCTGTAATCCCAGC
                                                                                                           ACTITGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCC
                                                                                                                                GTCGTGGGGCACCACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGTCACTTGA
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAR-2000;
07-JUN-2000;
28-JUN-2000;
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                            the cardiovascular system antigen polypeptides of the invention.

Cardiovascular system antigen polypeptides of the invention.

Cardiovascular system antigen and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral isohaemia, or nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungl, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, as offered and as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before
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Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                    Rosen CA, Barash SC, Ruben SM;
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           05-DEC-2000; 20000S-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
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2000US-0246474
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06-SEP-2000
08-SEP-2000
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
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(HUMA-) HUMAN GENOME SCI INC.

Ruben SM; Rosen CA, Barash SC,

WPI; 2001-451930/48.

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -

Claim 1; SEQ ID No 1943; 674pp; English.

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Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polymucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polymucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as carfiest, carebrovascular disorders such as carest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal

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------TAAAATATAAGCTGGGCTGGGCGGGGGCTCACACCTGTAATCCCCAGC, 15545
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        gastrointestinal disorders such as Crohn's disease, renal disorders such as a submaration partials and respiratory disorders such as astima and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin ading due to subburn, to maintain organs before transplantation, to regenerate tissues and in chemotasis.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of the printed at fitp.wipo.int/pub/published_pct_sequences.
premature labour and infertility
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Pred. No. 5.1e-64;
0; Mismatches 123; Indels 29;
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Best Local Similarity 78.6
Matches 558; Conservative
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chicken; sheep; immunosuppressive; antiarthritic; vasorropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; neoropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; described; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration;
horse;
Cardiovascular system antigen; human; mouse; rabbit; goat;
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2000US-0180628.
2000US-0184664.
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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17-MAR-2000;
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28-JUN-2000;
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23-AUG-2000;
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PR 14-SEP-2000; 20000S-0232399.
PR 14-SEP-2000; 20000S-0232399.
PR 14-SEP-2000; 20000S-0232399.
PR 14-SEP-2000; 20000S-0232309.
PR 14-SEP-2000; 20000S-02332409.
PR 14-SEP-2000; 20000S-02332409.
PR 21-SEP-2000; 20000S-023364.
PR 25-SEP-2000; 20000S-023409.
PR 25-SEP-2000; 20000S-023499.
PR 25-SEP-2000; 20000S-023499.
PR 25-SEP-2000; 20000S-023499.
PR 25-SEP-2000; 20000S-023499.
PR 25-SEP-2000; 20000S-02366.
PR 26-CCT-2000; 20000S-02366.
PR 27-CCT-2000; 20000S-02399.
PR 27-CCT-2000;
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Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Pred. No. 5.1e-64;
0; Mismatches 123; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 1944; 674pp; English.
                                                                                                                                                                                                                                                                                                   Ruben SM
                                   . 2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
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Best Local Similarity 78.6%;
Matches 558; Conservative 0
                                                                                                                                           2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
2000US-0251030
                                                                                                                                                                                                                2001US-0259678
                                                                                                                                                                                                                                                                                                Rosen CA, Barash SC,
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                                   05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
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05-JAN-2001;
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409 GTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGGCCTCCCGGGTTCACGCCATTCTCC

468

15151 TGTTCGTAACTCTTTTTTGTTGTTGTTAAGACAGACTCTTGCTCTGTCGCCCAGGCTGGA 15210

349 TTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGA

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529 TTTGTATTTTAGTAGAGGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGATCTCCTG

589 ACCTCGTGATCCGCCCCCCCCTCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCG

649 CGCCCGGCCATGATCATCTTCTTGACTATGCTGATGTGACAAGTACCTAAAGCCATCAGA 708

14 - AUG - 2000; 14 - AUG - 2000; 18 - AUG - 2000; 22 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 31 - AUG - 2000;	PR 01 SEP-2000; 200005-0229343. PR 01-SEP-2000; 200005-0229343. PR 01-SEP-2000; 200005-0229345. PR 05-SEP-2000; 200005-0229509. PR 05-SEP-2000; 200005-0229513. PR 06-SEP-2000; 200005-0231242. PR 08-SEP-2000; 200005-0231243. PR 08-SEP-2000; 200005-0231244. PR 08-SEP-2000; 200005-0231413. PR 08-SEP-2000; 200005-0231414. PR 08-SEP-2000; 200005-0231414.	PR 12-SEP-2000; 2000US-0232391. PR 14-SEP-2000; 2000US-0233401. PR 21-SEP-2000; 2000US-0233648. PR 22-SEP-2000; 2000US-0234391. PR 25-SEP-2000; 2000US-0234991. PR 25-SEP-2000; 2000US-0241809. PR 25-SEP-2000; 2000US-0241809. PR 25-SEP-2000; 2000US-0241809. PR 25-CCT-2000; 2000US-0234647
	AAAACG GCACAC ACACACAC GGCGGA III II GGCACACACACACACACACACACACACACACACACACAC	MALOSCOLY.  ALLOSCOLS standard; DNA; 12970 BP.  ALLOSCOLS.  ALLOSCOLS standard; DNA; 12970 BP.  ALLOSCOLS.  ALLOSCOLS.  ALLOSCOLS.  B. Human reproductive system related antigen DNA SEQ ID NO: 7689.  KW Human reproductive system related antigen; reproductive system disorder; w cancer; gene therapy; ds.  KW Human: reproductive system related antigen; reproductive system disorder; w cancer; gene therapy; ds.  KW Human: reproductive system related antigen; reproductive system disorder; w cancer; gene therapy; ds.  KW Human: reproductive system related antigen; reproductive system disorder; w cancer; gene therapy; ds.  KW Human: reproductive system related antigen; reproductive system disorder; w cancer; gene therapy; ds.  KW Human: reproductive system related antigen; reproductive system disorder; w cancer; gene therapy; ds.  KW Human: reproductive system related antigen; reproductive system disorder; w cancer; gene therapy; ds.  KW Human: reproductive system related antigen; reproductive system disorder; w colongs-0119626.  KW Human: reproductive system related antigen DNA SEQ ID NO: 7689.  KW Human: reproductive system related antigen; reproductive system disorder; w colongs-0119626.  KW Human: reproductive system related antigen DNA SEQ ID NO: 7689.  KW 17-JAN-2000; 2000015-0119626.  FR 11-JAN-2000; 2000015-011962.  FR 11-JAN-2000; 2000015-011963.  FR 11-JAN-2000;

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                                                                                                       6059 CTCCCGAGTAGCTGGGACTACAGGCGCCTGCCACCATGCCCGGCTAATTTTT--TATTT
                                                       6001 TIAGTAGACACAGGGTTTCACCGTGTTAGCCAGGATGGTCTCCATCTCCTGACCTCTGA
                                                                                                                                                                                                                                                               5711 GAAACCCTGTCTCTACTAAAAT-----ATAAAAATTAGCCATGCTGAC
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                                                                                                                                                                           658 ATGA-TCATCTTGACTATGCTGATGTGACAAGTACCTAAAGCCATCAGACTCTACCC
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                                       538 TTAGTAGAGACGGGTTTCACCGTTTTAGCCGGGATGGCCTCGATCTCCTGACCTCGTGA
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ID ABL97894 standard; DNA; 12970
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2000US-0180628.
2000US-0184664.
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04-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6179 TITITITITITITITITITAGAGACGAGTCTTGCACTGTCGCCCAGGCTGGAGTGCAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding a reproductive system antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12970 BP; 3310 A; 2917 C; 2938 G; 3805 T; 0 other;
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Pred. No. 5.8e-64;
0; Mismatches 197; Indels
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al Similarity 73.3%;
608; Conservative
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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01-08C-2000;
05-08C-2000;
05-08C-2000;
06-08C-2000;
08-08C-2000;
08-08C-2000;
08-08C-2000;
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08-DEC-2000
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The present invention provides the protein and coding sequences of 973
                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
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                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
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                                                                                   08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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22224
2000US-0186350
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I-AUG-2000;
I-AUG-2000;
                      19-MAY-2000;
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endothelin converting enzyme 1; ECE 1; EDNR;

Endothelin; EDN;

DNA encoding endothelin converting enzyme 1 (ECE-1) #2.

(first entry)

27-AUG-2002

ABK94412;

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               sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
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                                                                                                                                                                Gaps
 testicular antigens, and fragments of their genomic sequences.
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                                                                                                    Sequence 12970 BP; 3310 A; 2917 C; 2938 G; 3805 T; 0 other;
                                                                                                                                                             0; Mismatches 197; Indels
                                                                                                                                   Score 414.8; DB 2
Pred. No. 5.8e-64;
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ABK94412 standard; DNA; 74037 BP.

ABK94412/c ID ABK94 RESULT

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The invention describes a polynucleotide (I) of the endothelin

(EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

signaling system which is associated with a cardiovascular disease. (I),

the gene encoding EDN, ECE.or EDNR (II) or a vector (III) expressing (I),

or (II) is useful for producing cells capable of expressing a molecular

variant polypeptide which is associated with a cardiovascular disease.

(II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing

a molecular variant gene comprising (I) is useful for identifying and

obtaining a pro-drug or drug capable of modulating the activity of a

molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

or its gene product, or for identifying and obtaining an inhibitor of

the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

signaling system or its gene product. The isolated proteins and

polynucleotides encoding them are useful for preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to coronary angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolaemia. The gene or a polynuclectide fragment of the EDN/ECE/EDNR signaling system are useful as forensic markers, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ör
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          creating a transgenic animal and in creation of a solid support comprising polynucleotides, genes, vectors, polypeptides, antibodies host cells of the invention. This sequence encodes a fragment of the
                                                                                                                                                endothelin receptor; signaling system; cardiovascular disease; coronary heart disease; hypertension; atherosclerosis; anglogenesis; farty acid metabolism; diabetes; familial hypercholesterolaemia; forensic marker; transgenic animal; solid support; SNP; cardiovascular regulator; gene; ds; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotide of the endothelin/endothelin converting enzyme/receptors of endothelin and endothelin converting enzyme signaling system associated with cardiovascular disease, useful
                                                                                                                                                                                                                                                                                                                                                                                                                      "Single nucleotide polymorphism"
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2000US-0180628.
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2000US-0186350.
2000US-0189374.
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12-SEP-2000;
14-SEP-2000;
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    \times 2 \times 2 \times 2 \times 4 \times 5 \times 6 \times 5 \times 6 \times 5 \times 6 \times 7 \times 6 \times 6 \times 7 \times 6 \times 7 \times 7 \times 7 \times 6 \times 7 \times 7
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                                                                                                                                                                                                                                                                                   22531 TCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGAGGAGTCTCGCTCTGTTGCCCCAGGCT 22472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22231 CTGCGCCCGCCCTTTTTTTTTTTAAGGAAAATGGAAACTATTCATTTTTTTGAAATAA, 22172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAATTCCAGCACTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGAC 818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           879 TCAGCCGGGTGTCGTGGGGCACACCT-GTAATCCCAGCTATGCTGGAGGCTGAGGCACGA
cardioavscular regulator Endothelin converting enzyme 1 (ECE-1). Note: This sequence does not appear in the specification but has been obtained from GenBank using information given in the invention.
                                                                                                                                                                                                                                         346 TCTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCT
                                                                                                                                                                                                                                                                                                                                 406 GGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTC
                                                                                                                                            Score 414.6; DB 24; Length 74037;
Pred. No. 7.2e-64;
0; Mismatches 144; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 74037 BP; 18330 A; 19332 C; 19180 G; 17195 T; 0 other;
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                                                                                                                                            20.78;
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                                                                                                                                            Ouery Match 20.7
Best Local Similarity 77.1
Matches 550; Conservative
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959 CGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCCTGGGCGAC--AGAGCAA 1016
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                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9036 GCCGGGGTGGGCAGATTACCTGGGGTCAGGAGTTCAAGACCAGCCTGGTCAACATGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9096 AACCCCATCTGTACT------AAAAACACAAAAAATTTGCTGGCCATCGTGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 TAGTAGAGACGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGATCTCCTGACCTCGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8926 AGAATCTGCATTTTAAAAAATCCCCAGTTCTAAGTACAGGGGCATCTTAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        719 TAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8977 AAAATAAGAAATTTAGGCCTGGCGTGGTGGCTCAAGCCTGTAATCTCAGCA-TTTGGGAG
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                                                                                Isolated nucleic acid molecule encoding a reproductive system antigen
                                                                                                                                                                                                                                                                                                                                                                                                                               359 TTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        779 GCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                           Score 410.4; DB 22; Length 10445; Pred. No. 3.4e-63; 0; Mismatches 126; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1017 GACTCTGTCTCAAATAAATAAATAAACAAACGAACAAGCAGTTTGTTGTA 1066
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                                                                                                                                                                                                                                                                                                       Sequence 10445 BP; 2469 A; 2885 C; 2678 G; 2413 T; 0 other;
  Ruben SM
                                                                                                                                                                                                                                                                                                                                             20.5%;
78.9%;
                                                                                                                                                                                                                                                                                                                                             Query Match 20.5
Best Local Similarity 78.9
Matches 560; Conservative
  Rosen CA, Barash SC,
                                          WPI; 2001-465570/50
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                                                                           29-SEP-2000; 29-SEP-2000; 202-OCT-2000; 202-OCT-2000; 202-OCT-2000; 202-OCT-2000; 202-OCT-2000; 202-OCT-2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000
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AAL05001 standard; DNA; 12970 BP

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24; Gaps

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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                      Human reproductive system related antigen DNA SEQ ID NO: 7689.
                                                                                                                                                                                                                                                                                                                                            17-JAN-2001; 2001WO-US01339
                                           21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                      WO200155320-A2
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14-SEP-2000;
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AAL05001;
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6135
                                                                                                           testicular antigen; testes; cancer; metastasis; immune disorder;
1002 TGGGCGACAGAGCAAGAÇTCTGTCTCAAATAAATAAATAAACAAACGAACAAGCAGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human testicular antigen encoding DNA fragment SEQ ID NO: 2546
                                                                                                                                                     1062 TTGTACCTTAGTTATATCTAAAAA 1086
                                                                                                                                                                                                6196 TTGAGTTGTAGGAATTGCTTATATA 6220
                                                                                                                                                                                                                                                                                                          ABL97894 standard; DNA; 12970
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18-APR-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  942 CACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCC 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5797 GCCACCGCGCCTGGCCCGGCCCACATATTTTCGTTTGATAAGTATCTGTACAAATATTTT 5856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5910 TCCCAGAACTTTGGGAGGCCGAGGCGAGCAGATCAA--GAGGTCAGGAGATGGAGACCAT 5967
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATTTTTTTTTTTTAGTAGAGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 TCTCCTGACCTCGTGATCCGCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACCGCCCCGGCCATGATCATCTTGACTATGCTGATGTGACAAGTACCTAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           702 CATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  762 ITCCAGCACTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         882 GCCGGGTGTCGTGGGCCACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGT
                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTGGAGTGCAGTGCCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCTCCTGCCTCAGCTCCCAAGTAGCTGGGACTACAGGCGCCCCCCCACTACGCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.3%; Score 406.2; DB 22; Length 12970; Best Local Similarity 75.7%; Pred. No. 1.9e-62; Matches 564; Conservative 0; Mismatches 158; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 7689; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12970 BP; 3310 A; 2917 C; 2938 G; 3805 T; 0 other;
                                                                                                                                                                                                                                            Ruben SM;
                08-DEC-2000; 20000S-0251856.

08-DEC-2000; 20000S-0251868.

08-DEC-2000; 20000S-0251869.

08-DEC-2000; 20000S-0251989.

08-DEC-2000; 20000S-0251990.

11-DEC-2000; 20000S-02590.
                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
2000US-0251479
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                                                                                                                                                                                                                                                                                WPI; 2001-465570/50
                                                                                                                                                                                                                                            Rosen CA,
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2000US-0231418.
2000US-0231418.
2000US-0232081.
2000US-0232081.
2000US-0232398.
2000US-0232401.
2000US-0233063.
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
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5499 ATTITCITIGGITITITGGITTTTTTTTTTTTTGAGATGGAGTCTCGCTCTGTCGCCCA 5558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGGCCTCCCGGGTTCACGCC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAATTTTTTTTTTTTTTTTTTGTAGACGGGTTTCACCGTTTTTAGCCGGGATGGCCTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.3%; Score 406.2; DB 23; Length 12970; Best Local Similarity 75.7%; Pred. No. 1.9e-62; Matches 564; Conservative 0; Mismatches 158; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12970 BP; 3310 A; 2917 C; 2938 G; 3805 T; 0 other;
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                                                                                                                                                                                                    20000S-0249264
20000S-0249265
20000S-0249299
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20000S-0250160
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20000S-0250198
20000S-0256719
20000S-0256719
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2000US-0249244.
2000US-0249245.
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chronic colitis;
                                                                                                                                                            702 CATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAA
                                                     942 CACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCC
                                                                                                                                                                                                                            882 GCCGGGTGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; digestive system antigen; gene therapy; cancer;
ulcerative colitis; infection; Hirschsprung's disease;
digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGAGTTGTAGGAATTGCTTATATA 6220
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2000US-0184664.
2000US-0186350.
2000US-0189874.
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2000US-0205515.
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2000US-0215135.
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2000US-0224519
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24-FEB-2000;
02-MAR-2000;
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28-JUN-2000;
30-JUN-2000;
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07-JUL-2000;
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                                                                                                                                 TTGTATTTTTAGTAGAGACGGGTTTTCACCGTTTTTAGCCGGGATGGCCTCGATCTCCTGA
                                                                  CCTCGTGATCCGCCCCCCCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human digestive system antiquens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
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2000US-0249265.
2000US-0249297.
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2000US-0246532.
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Matches 553; Conserv
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Ruben SM 2000US-0241787. 2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-024221. 2000US-024617. 2000US-0246474. 20000S - 0246475 20000S - 0246476 20000S - 0246477 20000S - 0246523 20000S - 0246524 20000S - 0246525 20000S - 0246526 20000S - 0246527 20000S - 0246527 20000S - 0246527 200005-0249264. 200005-0249265. 200005-0249297. 200005-0249399. 200005-0249300. 200005-0251160. 2000US-0237040. 2000US-0239935. 2000US-0239937. 2000US-0240960. 2000US-0241785. 2000US-0241786. 2000US-0249207. 2000US-0249208. 2000US-0249209. 2000US-0249213. 2000US-0249214. 2000US-0249215. 2000US-0249215. 2000US-0249218. 2000US-0249244. 2000US-0249245. 2000US-0251030. 2000US-0251988. 2000US-0251988. 2000US-0251479. 2000US-0251856. 2000US-0251868. (HUMA-) HUMAN GENOME SCI INC 2000US-0246609 2000US-0246610 2000US-0246611 2000US-0246613 2000US-0249210 2000US-0249212 2000US-0249217 Rosen CA, Barash SC, WPI; 2001-541565/60 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 05-DEC-2000; 206-DEC-2000; 208-DEC-2000; 208-DEC-20000; 208-DEC-2000; 20 -NOV-2000; -NOV-2000; -NOV-2000; 17-NOV-2000; 17-NOV-2000; 01-DEC-2000; 01-DEC-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; L7 - NOV - 2000; 17-NOV-2000; 05-JAN-2001; 

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system , cancers and metastases -

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1341 AGGCTGCAGTGAGCC--GATCACACCACTGCACTCCAGCCTGGACAACAGAGTGAGACTC 1398
                                                                                                                                                                                                                       Human; prostate cancer antigen; cytostatic; uropathic; diagnositc; reproductive system; chromosomal marker; forensic; urinary disorder; chronic nephritis; blood-related disorder; thrombosis; ds.
                                                                                                                                                                                                DNA encoding human prostate cancer antigen, Seq ID No 668.
                         BP.
                                                                                                        N516/c
AAS40516 standard; DNA; 4433
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2000US-0184664
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06-SEP-2000;
06-SEP-2000;
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                                                                                                                                               The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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Pred. No. 2e-62;
0; Mismatches 167; Indels 21;
                                                                                                                                                                                                                                                                           Sequence 4433 BP; 1400 A; 857 C; 897 G; 1279 T; 0 other;
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14-SEP-2000
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The invention relates to novel isolated human prostate cancer antigen polynucleotides (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating, preventing and/ or prognosing disorders related to the reproductive nephritis; and blood-related disorders e.g. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in immunoassays. AAS40061-AAS40775 represent the human prostate cancer antigen coding sequences, and related PCR primers and sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 TTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGGGATCTCGG
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                                        2000US-0249297.
2000US-0249297.
2000US-0250160.
2000US-0250180.
2000US-0250391.
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2000US-0251479.
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2000US-0254097.
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2000US-0249265
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Matches 557; Conservative
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CGGCCTCCCA 	TCATCTTCTT	TCTTAACACT	ATATGCAGTT	GAATAAAGAA	GAGGTGGGTG	AAGGCGGGTG	TCTGTCTTA	GCCATCTCTA	CCTGTAATCC	TCTGTAATCC		AGGCTGCAGT	TGTCTCAAAT	TGTCTCAAAA	Search completed: August
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12908.483 Million cell updates/sec
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            GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 2971) Bepler,G. O'Briant,K.C., Kim,Y.C., Schreiber,G. and Pitterle,D.M. A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOHIIA metastasis suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699 AGCCATCAGACTCTACCCTTTAAATATGCAGTTGGGGCCAGGCACCGTGGCTCATGCCTG
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LOH11A
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Medicine and Radiology
Duke University Medical Center
Box 2610, MSRB, Room 117, Durham, NC 27710, part of a 1.4 megabase contig including the
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="11p15.5"
/clone="pTWB59.14"
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Class: unknown.
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ilarity 71.2%;
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Pred. No. 27;
0; Mismatches 119;
                    /organism="Homo sapiens"
nol_type="genomic DNA"
/db_xref="taxon:9606"
/map="11p15.5"
/clone="pTWB59.14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                   GCACAGTGGCGTGATYTCAGCTCGCTGCAACCTCTGCCTCCCGTGTTCAAGCAATTYTCC
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
17El: 81-438-52-3975
Fax: 81-438-52-3986
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Homo sapiens cDNA clone CS0DJ015YK20 3-PRIME, mRNA sequence.
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/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_tine="JURKAT"
/close_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Feb 16, 2001 this sequence version replaced gi:12946748. Contact: Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8901.f For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq-CsObJ015BF10NPl&cluster=8901.f. Contact
cgi.bin/cluster.cgi?seq-CsObJ015BF10NPl&cluster=8901.f. Contact
Feng Liang Email: fliang@lifetech.com/NL:
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSObJ015BF10NPl.
Location/Qualifiers
AGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCA
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Pred. No. 3.2e+02;
6; Mismatches 174; Indels 17; Gaps
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 500
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Clone distribution: MGC clone distribution information can.be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 43 Row: j Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                               Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chlu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hslao, Martin Krzyuinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schehn, Dunne Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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                  Direct Submission
Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1058 AGTGCAGTGGCGTGATCTCAGCTCACTGCAAGCTCTGCCTCCTGGGTTCAGGCCATTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACCTCATGATCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACC
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                                                                                                                                                                CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1641;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"taxon:9606"
/clone="IMAGE:5022014"
/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
                                                                                                   http://mgc.nci.nih.gov
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Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pOTB7"
364 c 447 g
                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                    Contact: MGC help desk
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                                                                                                    NIH-MGC Project URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1641
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1641)
                                                                                                                                                                                                                                                                                                                                                      ATGGCCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATT
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1. .652
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBB1000637"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
/note="Vector: pME18SFL3"
/ss a 161 c 163 g 167 t 6 others
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Pred. No. 6.9e+02;
0; Mismatches 125;
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Homo sapiens, clone IMAGE:5022014, mRNA
BC033224
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Best Local Similarity 75.7
Matches 494; Conservative
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Homo sapiens
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UI-H-DIO-avn-j-13-0-UI.sl NCI_CGAP_DIO Homo sapiens cDNA clone
IMAGE:5881836 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                        2412 CTCTGGCTAAATTAAATAGAAGATGAATTTACTGAAAAGTGTTATATGCCAGGAGTGGTG
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                                                                                                                                                                          -- ATCATCTTCTTGACTATGCTGATGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                              Indels
Score 336; DB 11;
Pred. No. 2.4e+02;
0; Mismatches 170;
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16.8%;
ilarity 73.2%;
Conservative
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Homo sapiens
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 Query Match
Best Local Similarity
Matches 549; Conserv
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Homo sapiens, Similar to hypothetical protein FLJ20489, clone
BC038630
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                                                                                                                                                                                                                  AACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCCTGGGCG 1007
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 2772)
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Submitted (15-OCT-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: i Column: 4 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.systemsblology.org
contact: amadan@systemsblology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
888 TGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGGTCACTTG
                                        CACTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGC
                                                                                                                                 99009----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CINA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:5263792"
/tissue_type="Brain, hippocampus"
/clone_lib="NHH_MGC_95"
/lab_host="DH10B"
/note="Vector: pBluescript"
623 c 602 g 865 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/CLONE_LSTORE THYMUS"
/Lissue_type="THYMUS"
/CLONE_LIb="HOMO saplens THYMUS"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                               ACTIGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCCT 1002
                                                                                                                                                                                                                                                                                                                                                                              630
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                                                                                                                                                                                                                                                              URL :
                                                                                         415 CCCAGTACTTCAGGAAGCCAAGGAGGGTGGATTCTTTGAGCCCAGAAATTCGAGACCAGG 474
                                                                                                                                          361 GAAGGACTGACGAGACTCACT-----GGTTGGCCGGGCGTGGTGACTCATATCTGAAAT 414
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                          763 TCCAGCACTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGC
                                                                                                                                                                                                                                     883 CCGGGTGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGTC
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Livrary was constructed by Life Technologies, a division of
Livrary was constructed by Life Technologies, a division of
Livrary was contact: Feng Liang Email: fliang@lifetech.com thtp://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPOO7CDOBQP1.
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251 c 231 g 249 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP007YH15"
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BX415714.1 GI:30654093
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//organism="Homo sapiens"
//mol_type="mina"
//mol_type="mina"
//mol_type="mina"
//db_xref="taxon:9606"
//clone="IMAGE:5881836"
//tissue_type="Lung Focal Fibrosis"
//dev_stage="Lung Focal Fibrosis"
//dev_stage="Lung Focal Fibrosis"
//dev_stage="Lung Focal Fibrosis"
//dev_stage="Lung Focal Fibrosis"
//doc=_lib="NCI_CGAP_DIO"
//note=="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
//note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
//clone_lib="Not I a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis: The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilgo-dry primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector: The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the Name of Maria II The sequence tag for this library is
         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this CDNA
sequence: 11-315, >ALU (matched compliment) 386-662, >ALU
POUTA-Yes.
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Pred. No. 7.2e+02;
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TAG_TISSUE-lung with fibrosis
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Best Local Similarity 71.1%;
Matches 517; Conservative
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                                                                                                                          /clone="CSODJ015YK20"
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/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
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                                                                                                                                                                                                           /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pcMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAACTGCATCTTTAACTTCGGCCGGGCAAGGTGGCTC--GCCTGTAATCCCAGCACTTT
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             http://fuillength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODJ015BF10NP1.
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                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606".
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Best Local Similarity 68.4%;
Matches 542; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 929)
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BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8901.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODJ015BF10NP1&cluster=8901.f. Contact
                             AGCCATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTG
                                                                                                                                                                                                                                                                                                                                                                                    AGTACAGTGGCATGATCACTGCAACCTCTGCCTCCCGGGTTCAAGGGATTCTT
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TTTATTTTTTATTTTTATTATTTTTTTTTTTTTTTGAGACCTAGCCTAGCTTGTCACCCAG
                                                                                                                                                             AATTTTTTTTTTTTTTTTTTGTAGAGGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGAT
                                                                                                                                                                                                                            CTCCTGACCTCGTGATCCGCCCCCCCCTCCCCAAAGTGCTGGGATTACAGGCGTGAG
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                                                                                          TTCTCCTGCCTCAGCTCCCAAGTAGCTGGGACTACAGGCGCCCCCCCACTACGCCCGGCT
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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KEYWORDS
SOURCE
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/clone="TWAGE:3837367"
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/lab_host="DHLOB (phage-resistant)"
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/cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE744242 11-SEP-2000 501576428F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837367 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 701)
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 666.
                                                                              301 TGCCTGGCCTTTTATTTTGTGTGTGTGTTTTGATTTCTGACTTGGCCTTTTTAAAAAAATC
                                                                                                                                                               709 CTCTACCCTTTAAATAIGCAGTTTGGGCCAGGCACCGIGGCTCAIGCCTGIAATICCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGTCACTTGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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Homo sapiens
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
/note="Vector: pME18SF13"
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Contact: Taxoa Isogai
Contact: Taxoa Isogai
Genomics Laboratory
Helix Research Institute
1153-3 Yana, Kisarazu, Chiba 292-0812, Japan
Far: 81-438-52-3975
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Submitted (15-OCT-2002) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Email: cgapbs rfemail.nih.gov
Itssue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTC Homo sapiens, Similar to hypothetical protein FLJ20489, INAGE:5263792, mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              852
                                                                                                                                                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 73 Row: i Column: 4
This clone has the following problem: retained intron.
Location/Qualifiers
                                                                             Anuradha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACTACGCCCGGCTAATTTTTTTTTTTTTAGTAGAGACGGGGTTTCACCGTTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCACTACGCCTGGCTGA--TTTTTTTTTTTTTTTTAGTAGAGGCAAGGTTTCACCATGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2394 CTATTTAATTTAGCCAGAGTTCACTTCTAACAAGCAAGATAGTTGATATATCAAGAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCTCTGTTGCCCAGGCT-GAGTGCAATGGTGTGATCTCGGCTCACTGCAACCTCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 CCGGGATGGCCTCGATCTCCTGACCTC - GTGATCCGCCCCGCCTCGGCCTCCCAAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAGGCTGG-TTTGAACTCCTGACCTCAGGTGACCTACCCGCCTCTCAAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        913 AGCTATGCTGGAGGCTGAGGCACGAGAGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TGATGTGACAAGTACCTAAAGCCATCAGACTCTACCCTTTAAATATGCAG--TTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCCAGGCACGCTCATGCCTGTAATTCCAGCACTTTGGGAGGCAGAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACTCTGTCTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAAAAAAAAAAAAAAAAAAAAAAAAATCAGCCGGGTGTCGTGGGGGCACACCTGTAATCCC
                                                                                                                                   þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Gaps
                                                                                               and Michelle Whiting
Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2772;
              DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Pahey, Erin Holton, Mark Ketteman, Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Wh
                                                                                                                                   Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5263792"
/clone=lib="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
/lab_host="DHI08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 321.6; DB 11;
Pred. No. 3.9e+02;
0; Mismatches 174;
The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                         : pBluescript"
602 g 865 t
Library Arrayed by:
                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%;
ilarity 72.4%;
Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 709)
E Hattori,M., Ishli,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
E Q bases 1 to 709)
E Q tases 1 to 709)
E J tases 1 to 709
E J tases 1 to 70
                                                           1889 AGCTGGGAGCAAATCCCCCCACCCCTACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGG 1948
                                                                                                                                                                                                                                                                                                                                                                                                         AGO10128 709 bp DNA linear GSS 14-APR-1999
Homo sapiens genomic DNA, 21q region, clone: f2G2X4, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 TGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGGGATCTCGGCTCACT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 GCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCTCCCAAGTAGCTGGGA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          675 TATGCTGATGTGACAAGTACCTAAAGCCATCAGACTCTACCCTTTAAATATGCAGTTTGG 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 TCACCATTTTAGCCGGGATGGTCTCGATCTTGACCTCGTGATCCGCCCCGCCTCGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                       GTGGCTCAGCAGGCAGGGAGGAGGTGTCTGTGCGTCCTGCACCCACATC 2000
                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 315.6; DB 29; Length
Pred. No. 1.4e+03;
0; Mismatches 139; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      φ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="21q"
/clone="f2G2X4"
179 c 184
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AG010128.1 GI:3294404
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al Similarity 73.3%;
499; Conservative
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Best Local 3
Matches 499
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AG010128
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TITLE
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GSS 28-APR-2003
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Cercopithecus aethiops

Bukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.

(bases 1 to 381)

Minhas,R., Zhang,X., Dore,C., Villeneuve,A., Lepage,P., Forgetta,V.,

MCRee,K., Ophoff,R.A., Fairbanks,L.A., Freimer,N.B., Ervin,F.R.,

Palmour,R.M., Hudson,T.J. and Dewar, K.

UCLA/MUGQ/St-Kitts Vervet Monkey Mapping Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1709 GGGGTGCTCTGGGGGTGGAGATAGGGGGAGCAGGAGGAGCTATTGCTAAGGCCCGATAGG 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCAGAGCCCAGGAGGAGGAGTGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTG 1888
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/dev_stage="white blood cell"
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/note="Vector: prakBAC2.1; Site_l: EcoR1; Site_2: EcoR1;
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/note="Vector: prakBAC2.1; Site_2: EcoR1; Site_2: EcoR1;
/note="Vector: prakBAC2.1; Site_2: EcoR1; Site_2: EcoR1; Site_2: EcoR
                                                                                                                                                                                                                                                                                                                CC061638
381 bp DNA linear GSS 28-APR-20
MUGQ_CH252P004Q3T7_M05_CD318_034 CHORI-252 Vervet Monkey Library
Cercopithecus aethiops genomic clone CH252-4B9, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            740 Dr. Penfield Room 7214, Montreal, QC, Canada, H3H 1A4
T=11: 514 398 3311 x00089
Fax: 514 398 1795
Email: S. Ren. dewar@mcgill.ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Dewar K
McGill University and Genome Quebec Innovation Centre
McGill University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cercopithecus aethiops"
"Mod_Lyppe="genomic DNA"
/db_xref="taxon:9534"
/clone="CH252-4B9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 4 row: B column: 9
Seg primer: T7: TAATACGACTCACTATAGGG
Class: BAC ends.
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                                                                                                                               AAATAAATAAACAAACGAACAA 1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC061638.1 GI:29790901
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with an cligc-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pyTYT3-Pac vector. The oligonucleotide used to prime the synthasis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The Sequence tag for this library is GTTAAGCGTC.

TAG\_LISB\_II-H-DFO

TAG\_LISB\_Subchondral bone

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// mol_type="mRNA"
// mol_type="mRNA"
// mol_type="mRNA"
// db_xref="I-H-DF0-ber-e-18-0-UI"
// tissue_type="Subchondral Bone"
// dev_stage="Adult"
// da_host="BHIOB (Life Technologies)"
// clone_ilib="NCI_GGAP_DF0"
// note="Organ: Bone: Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
// CGAP_DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this CDNA sequence: 11-300, >ALU (matched compliment) 366-655, >ALU 506-710,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA428305 710 bp mRNA linear EST 07-NOV-2002 UI-H-DF0-ber-e-18-0-UI.S1 NCI_CGAP_DF0 Homo sapiens cDNA clone UI-H-DF0-ber-e-18-0-UI 3', mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Umpublished
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TAG_SEQ=GTTAAGCGTC"
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PG-3 gene. PG-3 gene SE

EST-derived lung cancer

neuroblastom IL-1ra BAC c phospholipas immune/haema IL-1ra BAC c prostate exp flavin-conta

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Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
kallikrein-like protein; serine protease; cytostatic; cancer;
prostrate cancer; ds.
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          AAZ06260
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ACA04251
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                                                                The present sequence is the coding sequence of the human KLK-LZ gene, which encodes a kallkrein-like protein. Kallkreins and kallkrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kallkrein-like proteins KLK-LJ, KLK-LJ, KLK-LJ, KLK-LJ, KLK-LJ, KLK-LJ, KLK-LJ, KLK-LJ, KLK-LJ, MLK-LJ, MLK-LD, MLK-LB, have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostrate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used to treat conditions mediated by the kallikrein-like proteins.
                    treating KLK-L
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                   proteins for diagnosing and especially cancer. -
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                    (KLK-L)
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                   kallikrein-like
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                              1921 CTCTCTAGTTGAACCTGGGAACAATTTCCAAAACTGTCCAGGGCGGGGGTTGCGTCTCA
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, cosophageal; ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horrigan S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ebner R, Endress G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinoma, papillary carcinoma and Wilm's tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carter KC,
                                                      02-0CT-2000; 2000US-237295F-
02-0CT-2000; 2000US-237316F-
03-0CT-2000; 2000US-23758F-
03-0CT-2000; 2000US-23758B-
03-0CT-2000; 2000US-237604F-
                                                                                                                                                                                                                        03-0CT-2000; 2000US-237606P.
03-0CT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.
2000US-237278P
2000US-237294P
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Best Local Similarity 100.
Matches 482; Conservative
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the convextuant of cancer such as colon, breast, stomach, lung, thyrold, ossophageal, ovarian, kidney, prostate or pancreatic cancer, additional cancer, infiltrating ductal cancer, infiltrating ductal cancer, additional cancer, and convextuant of cancer such as a colon, and cancer and convextuant of cancer cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1650 GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC 1709
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                                                                                                                                                                                                                                                                      Endress G,
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                                                                                                                                                                                                                                                                         Carter
                         2000US-237604P.
2000US-237606P.
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                                                                                                                                                                                                              (AVAL-) AVALON PHARM
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                                                           03-OCT-2000;
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01-NOV-2000;
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                                                                                                                                               2010 TCAGGGCCCATCCCTTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGA 2069
                                                                                                                                                                                  Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
                                                        141 CAAAACTGTCCAGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
                               CAAAACTGTCCAGGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast cancer related gene sequence SEQ ID NO:2333.
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ID ABL63996 standard; DNA; 586 BP.
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2000US-233617P.
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   320 CCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTC 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides, useful for treating response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that bind to a breast tumour polypeptide, detecting in the sample an amount of polypeptide to a predetermined cut. off value, therefore determining the presence of a cancer in the patient. Sequences ABK28020-BKK29025 represent cDNA clones encoding human breast tumour polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic;
                                 1830 CCAGAGATGTTGAGAATGTTCATCTCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGG
                                                 260 CCAGAGATGTTGAGAATGTTCATCTCTCTCAGCCCTGACCCCATGTCTCTCTGGGCTCAGG
                                                                                           1890 GTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCTGGGAACAATTTC
                                                                                                             200 GTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGGGAACAATTTC
                                                                                                                                                      1950 CAAAACTGTCCAGGGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retter MW, Harlocker SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human breast tumour polypeptide cDNA clone #42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 140; 150pp; English.
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12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant.
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AG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy and diagnosts of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel isolated polypeptide comprising an immunogenic portion of a breast cancer protein useful in the detection and treatment of breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                          Human; breast tumour antigen; cytostatic; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 735 BP; 161 A; 176 C; 226 G; 172 T; 0 other;
                                                                                                                                                                                                                                               tumour clone B541S.
                                                                                                                                                      BP.
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                                                                                                                                                                                                                                             CDNA sequence of human breast
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ID AAC79469 standard; cDNA; 735
                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0288950
99US-0346327
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                                                                                                                                                                                                                                                                                          breast cancer; vaccine; ss
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Best Local 3
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1650 GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC 1709
                                                                                            This sequence encodes a human breast tumour protein immunogenic fragment of the invention. The polypeptides or nucleic acids encoding them are useful in vaccines and pharmaceutical compositions for manufacture of medicaments for inhibiting the development of breast cancer in a patient. They can also be used to treat breast cancer. Antibodies against these polypeptides can be used to detect and monitor progression of breast polypeptides can be used to detect and monitor progression of breast encoding the breast proteins are useful for detection of breast cancer. Peripheral blood cells from a patient incubated in the presence of at least one polypeptide, such that T cells proliferate, are useful in manufacture of a medicament for treating breast cancer in a patient. Antigen presenting cells incubated in the presence of at least one polypeptide are also useful for treating breast cancer.
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                         breast tumour protein genes used, in vaccines for immunotherapy
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                                                                                                                                                                                                                                                                                                                                         Length 738;
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100.0%; Pred. No. 5.7e-81;
live 0; Mismatches 0;
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                                          for diagnosis of breast cancer
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                                                                       Claim 3; Page 70; 70pp; English.
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Matches 482; Conservative
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                              protein; immunogenic fragment; vaccine; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding human breast tumour protein immunogenic fragment.
                             24; Length 735;
                                                           Indels
Sequence 735 BP; 161 A; 176 C; 226 G; 172 T; 0 other;
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                             Score 482; DB 24;
Pred. No. 5.7e-81;
                             23.3%; Score 482; DB
ilarity 100.0%; Pred. No. 5.7
Conservative 0; Mismatches
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97US-0998253.
97US-0998255.
98US-0118554.
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                             Query Match
Best Local Similarity
Matches 482; Conserv
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breast cancer
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24-DEC-1997
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AAX84240/c
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1590 CAGGGTGATTCTGGGGGCCCTGTGGTCTGCAATGGCTCCTGCAGGGACTCGTGTCCTGG 1649
                                                                                                     1231 TCAGGGCCCATCCTTCTCTGCAGCTCTGACCCCAAATTAGTCCCAGAAATAAACTGAGA 1290
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The invention relates to a method of detecting the presence of a target BS247 polynucleotide, especially mRNA, in a test sample. BS247 polynucleotides are derived from breast tissue. The polynucleotides, polynecleotides are useful for providing information leading polypeptides or antibodies are useful for providing information leading imging, prevention, diagnosis, staging, monitoring, prognosis, in vivo imaging, prevention or treatment, determining predisposition to, diseases and conditions of the breast, such as breast cancer, atypical hyperplasia, fibroadenoma and cystic breast disease. Drug treatment or perest cancer, can be based on these identified gene sequences and the efficacy of any particular therapy can be monitored. The BS247-derived reagents are advantageous for detection of breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer due to their specificity. The reagents also provide an alternative, non-surgical diagnostic method capable of detecting early
                                      1171 CAAAACTGTCCAGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
1950 CAAAACTGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
                                                                                   2010 TCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGA
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Hodges SC, Klass MR, Kratoch
Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1302 BP; 281 A; 413 C; 338 G; 270 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibroadenoma; cystic breast disease; gene therapy; ss.
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Pred. No. 6.1e-81;
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                                                                                                                                                                                                                                                                                                                        AAX57990 standard; DNA; 1302 BP.
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97US-0063431.
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, Stroupe SD,
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                                                                                                                                                                       AG 2071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Russell JC,
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Best Local Simi
Matches 482;
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The invention relates to a method of detecting the presence of a target BS247 polynucleotide, especially mRNA, in a test sample. BS247 polynucleotides are derived from breast tissue. The polynucleotides, proposed from breast tissue. The polynucleotides or antibodies are useful for providing information leading polynucleotides or antibodies are useful for providing information leading to the detection, diagnosis, staging, monitoring, prognosis, in vivo imaging, prevention or treatment, determining predisposition to, diseases and conditions of the breast, such as breast cancer, atypical hyperplasia, fibroadenoma and cystic breast disease. Drug treatment or gene therapy for breast cancer, can be based on these identified gene sequences and the efficacy of any particular therapy can be monitored. The BS247 derived reagents are advantageous for detection of breast cancer due to their specificity. The reagents also provide an alternative, non-surgical diagnostic method capable of detecting early stage breast disease, such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1590 CAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCTGG 1649
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               BS247; detection; diagnosis; breast cancer; atypical hyperplasia; fibroadenoma; cystic breast disease; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                              M, Colpitts TL, Friedman PN;
Hodges SC, Klass MR, Kratochvil JD;
Yu H;
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Pred. No. 6.1e-81;
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100.0%; Pred. No. v...
... 0; Mismatches
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97US-0063431.
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                                                                                                                                                                                                                                                                                                                                                                                       Granados EN,
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                                                                                 Homo sapiens.
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28-OCT-1997;
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Human secreted protein gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; osteoperate; destroying, prostate; obesity; osteoclast; thymus; osteoperasis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                1111 GTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTTAGTTGAACCCTGGGAACAATTC
                             ACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACA
                                                                   CCAGAGATGTTGAGAATGTTCATCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGG
                                                                                                                                            CAGGGTGATTCTGGGGGGCCCTGTGGTCTGCAATGCCTCCTGCAGGGACTCGTGTCCTGG
                  GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC
                                                                                              CCGGCATCCCCACCTGCTGCAGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTC
                                                                                                                                                                        GTCTGCTTCCCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGGGAACAATTTC
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Soppet DR;
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Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein gene No.
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98US-0070658.
98US-0070692.
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Rosen CA,
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07-JAN-1998;
07-JAN-1998;
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human humunoglobulin FC portion (e.g. Az206210) for increasing the stability of the fused protein as compared to the human protein only The invention relates to 36 novel genes and their fragments (nucleic acid sequences: Az206219-206263; amino acid sequences AX38386-Y38438) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polymprides in a sample or by determining the presence of mutations in polymprides in a sample or by determining the presence of mutations in polymbrotides, based on which issues are described for each of the 36 polymbrotides, based on which issues they are most highly expressed in (see AAZ06219 for described uses).
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100.0%; Pred. No. 6.1e-81;
iive 0; Mismatches 0;
                                                           Claim 1; Page 173-174; 227pp; English.
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Best Local Similarity 100.
Matches 482; Conservative
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1150 CCAGAGATGTTGAGAATGTTCATCTCTCCAGCCCCTGACCCCATGTCTCTGGACTCAGG 1209
                                                                                                                                                                                               This DNA encodes a human keratinocyte derived protease (KDP) polypeptide. The protease is substantially similar to a sequence encoded by the insert in plasmid FERM BP-6129. The KDP polypeptide, from human keratinocytes, is specifically used in skin care products, particularly to treat or prevent skin flaking, e.g. dandruff, and in laundry detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keratinocyte derived protease; KDP; protease; keratinocyte; human;
skin care product; skin flaking; dandruff; laundry detergent composition;
cleaning composition; dishwashing product; ss.
                                                                               1210 GTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTTAGTTGAACCCTGGGAACAATTTC
                                                                                                                                1270 CAAAACTGTCCAGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
                                                                                                                                                                              2010 TCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGA
                                                                                                              1950 CAAAACTGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human keratinocyte derived protease (KDP) encoding DNA
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                            diagnosis; tissue, cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal defliciency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAZ06210) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (nucleic acid sequences: AAZ06219-Z06263; amino acid sequences AAX38386-Y38498) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucletides in a sample or by determining the presence of mutations in the new polypucletides. Specific uses are described for each of the 36 the 36 the manner of the new polymorectides.
                    gene therapy; protein therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a nucleic acid molecule which encodes a
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Pred. No. 6.2e-81;
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100.0%; Pred. No. ...
0; Mismatches
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Soppet DR;
                  secreted protein; fusion protein;
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                                                                                                                                                                                                                                                                                                                                                                                                          Ebner R,
Ruben SM,
                                                                                                                                                                                                                                                                                         98US-0070704.
98US-0070657.
98US-0070658.
98US-0070692.
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Rosen CA,
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                                                                                                                                                             Homo sapiens
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07-JAN-1998;
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Rosen CA,
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P-PSDB; AAY38412.
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        07-JAN-1998;
07-JAN-1998;
07-JAN-1998;
                                                              Brewer LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; fusion protein; gene therapy; protein therapy;
                                                                            1314 GTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCTGGGAACAATTC
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can be used in
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                                            Length 1499;
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compositions. More generally the KDP polypeptide can be
cleaning composition, e.g. hard surface or dishwashing
                         322 T; 0 other;
                                                    6.2e-81;
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                                          DB 20;
                                         23.3%; Score 482; DB
100.0%; Pred. No. 6.2
:ive 0; Mismatches
                         Sequence 1499 BP; 310 A; 469 C; 398 G;
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                                                   Local Similarity 100. nes 482; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AA206210) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (nucleic acid sequences: AA206219-206263; maino acid sequences AA718386-Y38498) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypurcleotides. Specific uses are described for each of the 36 polynucleotides, based on which tissues they are most highly expressed in
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100.0%; Pred. No. 6.2e-81;
ive 0; Mismatches 0;
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Soppet |
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98US-0070704.
98US-0070657.
98US-0070658.
98US-0070692.
                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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Ruben
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Best Local Similarity 100.
Matches 482; Conservative
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980S-0090429
980S-0090431
980S-0090445
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98US-0090863.
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                                                                                                                                   Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.
                                                                                                        Membrane-bound protein PRO1132 encoding cDNA.
                          AAZ65070 standard; cDNA; 1570 BP
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98US-0087759.
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98US-0088021.
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                                                                               05-APR-2000
                                                                                                                                                                            Homo sapiens
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                                                     AAZ65070;
RESULT 13
AAZ65070
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1437 CAAAACTGTCCAGGGGGGGGTTGCGTCTCAATCTCCCTGGGGGCACTTTCATCCTCAAGC 1496
                               TCAGGGCCCATCCCTTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGA 2069
                                              Human secretory and transmembrane; PRO; mammalian; cancer; lung; braast; prostate; cervical; tumour necrosis factor-alpha; TMR-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deforge L, Desnoyers L, Filvaroff E, (
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                             Human cDNA sequence encoding for PRO1132 polypeptide.
                                                                                                                                                                                                     AAS21471 standard; cDNA; 1570 BP
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99WO-US28551
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99US-0170262
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Smith V, Stewart TA, Tum
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AG 1558
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                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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20-MAR-2000;
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30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, on be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO
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                                                                                                                                                                                                                                                     Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.3%; Score 482; DB 21;
100.0%; Pred. No. 6.2e-81;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                       Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 225; 822pp; English.
                                                                                                                                                                                                                                                     Goddard A,
                                                    98US-0097955.
                                                                                  98US-0097974
98US-0097978
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98US-0098014
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99US-0115565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by recombinant techniques.
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                                                                                                                                                                                                                          (GETH ) GENENTECH INC
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P-PSDB; AAY66726.
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Yuan J;
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Matches 482;
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26-AUG-1998
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The Probability of the Probabili
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                                                                                                                                 encode for novel human secretory and transmembrane
  presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antisense RNA/DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO polypeptides can be used to generate probes, antisense RNA/I
transgenic or knock out animals and can be used in gene therapy.
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and detect the
                                                                            813pp; English.
                             lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
  polypeptides,
                                                                            Fig 455;
                                                                                                                               AAS21244-AAS21518
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                                                                          Claim 3;
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AAF44216 standard; cDNA; 1570 BP.

RESULT 15
AAF44216
ID AAF4

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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for trargeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DL;
Godowski PJ;
Paoni NF;
Wood WI;
                                                                                     Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
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Berrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                          Human PR01132 (UNQ570) nucleotide sequence SEQ ID NO:308.
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2000WO-US03565.
2000WO-US04341.
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CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT PLING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11-12
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Patent No. 6478825
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APPLICATION NUMBER: 60/087827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                   Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy, Margaret Ann
Stewart, Timothy
Tumas, Daniel
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Serritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [javin, Ivar J
                                                                                                                                                                                                                                                                                                                                Botstein, David
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Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                     ong, Sherman
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20 AG 19
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60/088167

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1590 CAGGGTGATTCTGGGGGCCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCTGG 1649
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                            1137 GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC
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                                                                                                          1650 GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC
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APPLICANT: Hillman, Jennifer L.

APPLICANT: ADI, Preeti

TILLE OF INVERTION: NOVEL KALLIKREIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto
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REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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| AG 1558
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US-08-824-874-2
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                    R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089952
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-23
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R APPLICATION NUMBER: 60/090690

R APPLICATION NUMBER: 60/090690

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090694

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090695

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090862

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090862

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26
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RELIGNE DATE: 1998-07-01
RELIGNE DATE: 1998-07-01
RELIGNE DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                            R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090678
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-07-09
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                    PRESENTATION OF PRESENTATION O
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1650 GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC 1709
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100.0%; Pred. No. 1.4e-90;
ive 0; Mismatches 0;
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STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/824,874
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Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                   ATTORNEY/AGENT INFORMATION:
NAME: B1111095, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                    LENGTH: 1476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                   TELEFAX: 415-845.4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.°
Matches 476; Conservative
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COUNTRY: USA
ZIP: 94304
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CLONE: 820694
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US-09-764-762-2
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                                                                                                                                                                                                                                                                                                                                           1650 GGAGATTACCCTTGTGCCCGGCCCAACAGACGGGTGTCTACACGAACCTCTGCAAGTTC 1709
                                                                                                                                                                                                                                                                                                                                                              1710 ACCAAGIGGAICCAGGAAACCAICCAGGCCAACTCCIGAGTCAICCCAGGACICAGCACA 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1770 CCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTC 1829
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                                                                                                                                                                                      Length 1476;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                      Query Match 23.0%; Score 476; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Freeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09210084
Patent No. 6197511
                     LENGTH: 1476 base pairs
 SEQUENCE CHARACTERISTICS
                                   TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                               KERANOT02
                                                                          linear
                                                        STKANCL...
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANO
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CITY: Palo Alto
STATE: CA
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ 1D NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                       Human Protease
                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                          Length 1504;
                       Encoding
                                                                                                                                                                                                                                                                                    Score 460; DB 4; 1
Pred. No. 3.1e-87;
0; Mismatches 0;
                                                                                                                                                                                                                                ; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-1
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules J.
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILIG DATE: 1999-03-26
SOFTWARE: PALCHING DATE: 2099-03-26
SOFTWARE: PALCHIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09128155 Patent No. 6117654
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99.6%;
                                                                                                                                                                                                                                                                                        Query Match 22.2
Best Local Similarity 99.6
Matches 482; Conservative
                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                     LENGTH: 1504
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                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.0%; Score 476; DB 4;. Best Local Similarity 100.0%; Pred. No. 1.4e-90; Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF-0252 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <u >Unknown></u>
                                                                                                                                                                                    APPLICATION NUMBER: 09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                        FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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US-09-280-116-1
Sequence 1, Application US/09280116A; Patent No. 6331427; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1476 base pairs
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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CLONE: 820694
                                                                                                                                                                   PRIOR APPLICATION DATA:
COMPUTER READABLE FORM
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                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: AND USES THEREOF
TITLE REFERENCE: 094.04.52001
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-08-03
EARLIER PILING DATE: 1998-08-07
EARLIER PLING DATE: 1998-08-07
EARLIER PLING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SEQ ID NOS: 18
SEQ ID NOS: 18
SEQ ID NOS: 18
                                                                                                                                         1058 AAAGGTTGAACTTGGAGGCCAGGCATGGTGGCTCACGCCTGTAATCCCAACACTTTGGAG
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Pred. No. 1.4e-36;
0; Mismatches 58;
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                                                                                                                                                                                                                                                                                  ; Sequence 16, Application US/09128155 ; Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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Best Local Similarity 81.4%;
Matches 254; Conservative
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US-09-326-480A-4
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APPLICANT: C. Frank Bennett
APPLICANT: C. Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                         36312 TCACCTGAGGTTAGGAGTTCGAGACCAACCTGGCCAACATGGTGAAACCCCGTCTCTACT 36253
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Pred. No. 1.1e-36;
0; Mismatches 41;
                                                                                                                                                                                                   Score 222.6; DB 3;
Pred. No. 2.9e-37;
0; Mismatches 49;
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                                                                                                 NAME/KEY: misc_feature

// LOCATION: (1)...(176373)

// OTHER INFORMATION: n = A/T,C or

US-09-128-155-17
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Best Local Similarity 84.0%;
Matches 263; Conservative
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Best Local Similarity 85.95
Matches 255; Conservative
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ORGANISM: Homo sapiens
                                       TYPE: DNA
ORGANISM: Homo sapiens
                      LENGTH: 176373
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LENGTH: 70000
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US-09-851-896-3
    SEQ ID NO 17
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                                                                                 FEATURE:
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Query Match
Best Local Similarity
Matches 255; Conserv
                              Best Local Similarity
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US-09-404-879A-3/C
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                         APPLICANT: Henri-Jean Garchon
APPLICANT: Henri-Jean Garchon
APPLICANT: Jean-Francois Bach
TITLE OF INVENTION: NOLEGOTIBE SEQUENCE WHICH ENCODES A
TITLE OF INVENTION: ELAVIN MONOCYCERNASE, THE CORRESPONDING PROTEIN AND THEIR
TITLE OF INVENTION: USES IN THE SPHERES OF DIAGNOSIS AND THERAPY
TITLE OF INVENTION: USES IN THE SPHERES OF DIAGNOSIS AND THERAPY
TITLE OF INVENTION: USES IN THE SPHERES OF DIAGNOSIS AND THERAPY
CURRENT PELLICATION NUMBER: US/09/326,480A
PRIOR APPLICATION NUMBER: PCT/FR97/0226
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1996-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACAAAAAAATACAAAAATTAGCCGGGTGTGGTGATGGACACCTGTAGTCACAGCTAC 1248
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APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REPERBACE: 210.11.4622.2
CURRENT APPLICATION NUMBER: US/09/404,879A
NUMBER OF SEQ ID NOS: 393
SOFTWARE: PASSEQ FOR Windows Version 3.0
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Pred. No. 1.3e-36;
0; Mismatches 44
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 25464
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; Sequence 1, Application US/09404879A
; Patent No. 6468546
                                                                                                                                                                                                                                                                                                                                                                                    10.6%;
85.0%;
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APPLICANT: Marta Blumenfeld
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Best Local Similarity 85.0'
Matches 256; Conservative
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
UNMBER OF SEQ ID NOS: 393
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  Length 461;
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DB 4;
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                    .5e-36
                    Pred. No. 1.5e
0; Mismatches
Score 216.4;
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  10.48;
                    84.48;
                                     Conservative
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Patent No. 6528253

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS

TITLE OF INVENTION: OF OVARIAN CANCER

FILE REFERENCE: 210121.463

CURRENT APPLICATION NUMBER: US/09/215,681A
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                                               Score 216.4; DB 4
Pred. No. 1.5e-36;
0; Mismatches 46
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Pred. No. 1.5e-36;
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SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 84.4%;
Matches 255; Conservative
                                              Query Match 10.4%;
Best Local Similarity 84.4%;
Matches 255; Conservative
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ORGANISM: Homo sapien
; ORGANISM: Homo sapien US-09-338-933-3
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US-09-215-681-1/c
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APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.46201
CURRENT APPLICANTION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
                                                                                                                                                                                                        APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
SUTRENT FILING DATE: 1999-06-23
SUTRENT FILING DATE: 1999-06-23
SOFTWARE: FASTERQ for Windows Version 3.0
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Patent No. 6488931
                                                                                                                                                        Sequence 1, Application US/09338933 Patent No. 6488931
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-Q=/cgn2_1/USPTO_spool/US09936271/runat_04082003_104245_25702/app_query.fasta_1.455
-Q=/cgn2_1/USPTO_spool/US09936271/runat_04082003_104245_25702/app_query.fasta_1.455
-DB-GenEmbl. OFWT=fastap - SUFFXX=reg - MINMATGH=0.1 - LOOPCLD.0 - LOOPEXT=0
-UNITS-blts START=1 - END=-1 - MATRIX=Dosum62 - TRANS=human40.cd1 - LIST=45
-DOCALIGN=200 - THR_SCORE=pct - THR_MXX=100 - THR_MIN-0 - ALIGN=15 - MODE=-LOCAL
-OUTFWT=pto - NORM-ext - HEAPSTIZE=500 - MINLEN=0 - MAXEN=200000000
-USFR-US09936271_GCGN_1_1_2326_Grunat_04082003_104245_25702.NCPU=6 - ICPU=3
-NO_MMAP - LARGEQUERY - NEG_SCORES - WAIT - DSPBLOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FCAPOP=6
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Staline, N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Woreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission

Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned wising BD In-Fusion(TM)
cloning system between the Sall and Hindill sites of the pDNR-DDAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'Hid III site to maintain reading frame.
Clone distribution: http://Dioinfo.clontech.com/orfclones.
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-RATRAPKRONRPINVSSHCPRSCQAGDSGGPVCHVSPWCOLNISVEGREE
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                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 882)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Rounding,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
                  PRI 13-MAY-2003
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collection"
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/note="Vector: pDNR-Dual"
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          882 bp mRNA lir
Homo sapiens kallikrein 5 mRNA, complete cds.
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FLI_CDNA.
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Homo sapiens
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AUTHORS
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KEYWORDS
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AX279380 1370 bp mRNA linear PRI 26-MAY-2003
Homo sapiens kallikrein 5 splice variant 1 (KLK5) mRNA, complete
cds; alternatively spliced.
AX279380.1 GI:31075480
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Kurlender, L., Yousef, G.M., White, N.M.A., Robb, J.-D., Borgono, C.A. and Diamandis, E.P.

Direct Submission

Submitted (19-APR-2003) Pathology and Laboratory Medicine, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
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                                                                                                                                  CCCCACCCTGGCTACTCCCACCCTGGCCACCTCTAACGACCTCATGCTCAAACTGAAC
                                                                                                                                                                                   ArgarglleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer
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Kurlender,L., Yousef,G.M., White,N.M.A., Robb,J.-D.,
and Diamandis,E.P.
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    1370
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                                                          L. Submitted (13-MAY 2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and Hindill sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before Affic to provide Kozak consensus sequence; 'GG' after last codon and before Hindill site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                          1. .>882
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DAYPROIDDYMRAGGRAGRAGRAGRAGRAGRAGGTTKSPQVHFPKVLQCLNISVLSQKRCE
DAYPROIDDYMRAGGRAGRAGRAGRAGRAGRAGGTTKSPQVTT
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koudinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
Direct Submission
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/note="Vector: pDNR-Dual"
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                                                                                                                                                                                                                                                                                                               PAT 18-SEP-2002
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Eukaryotain Metazoa (Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 1381)
Ruben, S. M., Soppet, D. R., Ebner, R., Lafleur, D. W., Ni, J.,
Brewer, L. A., Olsen, H. S., Duan, R. D. and Rosen, C. A.
Batent: JP 2005500035-A 50 08-JAN-2002;
HUMAN GENOME SCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC A61P37/00,C07K14/435,C07K16/18,C12N1/15,C12N1/21,C12N5/10,C12N15/00,C12N15/00,C12N15/00,CC 36 human secreted proteins
FH Key Location/Qualifiers
           PF 06-JAN-1999 JP 2000527554
PR 07-JAN-1998 US 60/070658,07-JAN-1998 US 60/070658
07-JAN-1998 US 60/070652,07-JAN-1998 US 60/07074 PI M RUBEN, DANIEL R SOPPET, REINHARD EBNER, DAVID W LAFLEUR, PI
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a 425 c 353 g 274
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36 human secreted proteins.
BD107879 161:23202697
JP 2002500035-A/50.
Homo sapiens (human)
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JP 2002500035-A/50
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E 2 (bases 1 to 1387)

Brattsand, M. and Egelrud, T.

Direct Submission

Dermatology and Venereology, Umea University, University Hospital, Unes SE-901 85, Sweden

E Brattsand, M. and Egelrud, T.

Brattsand, M. and Egelrud, T.

Direct Submission

L Dermatology and Venereology, Umea University, University Hospital, Direct Submission

L Submitted (16-APR-2002) Public Health and Clinical Medicine, Dermatology and Venereology, Umea University, University Hospital, Umea SE-901 85, Sweden

Sequence update by submitter

C Sequence update by submitter

C NAT 16, 2002 this sequence version replaced gi:6063032.
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                                             human stratum
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   Euteleostomi;
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function in
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  Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I (bases I to 1387)
Brattsand, M. and Egelrud, T. Purification, molecular cloning, and expression of a corneum trypsin-like serine protease with possible;
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                              CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260
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                                                                        LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn
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Homo sapiens kallikrein 5 splice variant 2 (KLK5) mRNA, complete
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Kurlender, L., Yousef, G.M., White, N.M.A., Robb, J.-D., Borgono, C.A. and Diamandis, E.P.
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2 (bases 1 to 1438)
Yousef,G.M., Robb,J.-D., White,N.M.A., Kurlender,L., Borgono,C.A. and Diamandis,E.P.
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Submitted (19-APR-2003) Pathology and Laboratory Medicine, Mount
Sinal Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
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                       TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle
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Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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C12N15/57,C12N9/64,A61K38/48,A61K7/48,C11D3/386,C07K16/40
                916 TGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCTGCAGGGACTCGTGTCC
                                         AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe
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Kitado, H., Yoshikawa, A. and Zaiki, T.
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/organism="unidentified"
/mol_type="genomic DNA"
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Homo sapiens, kallikrein 5, clone MGC:1107 IMAGE:2989806, mRNA,
complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6912643.
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTP/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanésystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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                                                                                                                                                                                                                                                                                                                                                AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1536)
Strausberg, R.
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/mol_type="mRNA"
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PN JP 2002500035-A/36
PD 08-JAN-2002
PP 06-JAN-1999 JP 2000527554
PR 07-JAN-1998 US 60/070657,07-JAN-1998 US 60/07065
07-JAN-1998 US 60/070692,07-JAN-1998 US 60/0707069
M RUBEN, DANIEL R SOPPET, REINHARD EBNER, DAVID W LAFLEUR, PI
              Ruben, S.M., Soppet, D.R., Ebner, R., Lafleur, D.W., Ni, J., Brewer, L.A., Olsen, H.S., Duan, R.D. and Rosen, C.A. Brewer, L.A., Olsen, H.S., Duan, R.D. and Rosen, C.A. Batentan secreted proteins Patent: JP 2002500035-A 36 08-JAN-2002; HUMAN GENOME SCIENCES INC S Homo sapiens (human) PN JP 200250035-A/36 PD 08-JAN-2002
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/organism='Homo sapiens (human)'.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer
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Minterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
Implant, method of making same and use of the implant for treatment of bone defects
treatment of bone defects
Patent: US 6478825-A 308 12 NOV-2002;
Location/Qualifiers
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Sequence 308 from patent US 6478825.
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DAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCNGSLQGLVSWGDYPCARPNRPGVYT
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TACTCCCTGTCACCAGTTTATGAATCTGGGCAGAGATGTTCCAGGGGGTCAAATCCATC 773 ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 160	oy Qy	154 ATGCTACAGCAAGACCCCCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTT 21 LeuGlyValthrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn
ArgargileargprothrlysaspvalargproileasnvalserSerHisCysProSer 180 	oy da	41 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60
AladiyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 200 	QY da ,	61 AspAspSerSerArgileileAsnGlySerAspCysAspMetHisThrGlnProTrp 80
ProlysvalleugincysleuasnileServalleuSerginlysArgCysgluaspala 220 	Oy Do	81 GlnalaalaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro 100
TyrProargGln11easpaspthrMetPheCysalaGlyaspLysAlaGlyargaspSer 240 	Oy Db	101 GlnfrpleuleuthralaalaHisCysarglysLysValPheargValargleuGlyHis 120 
CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260 	QQ QQ	121 TyrserLeuserProvalnyrGluserGlyGlnGlnMetPheGlnGlyValLysserIle 140 
Trp6lyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys 280	QY	141 ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeu1leLysLeuAsn 160 
PheThrLysTrpileGlnGluThrileGlnAlaAsnSer 293	QY Db	161 ArgargileargProThrLysAspValargProlleasnValSerSerHisCysProSer 180 
1570 bp DNA linear PAT 27-FEB-2001	Qy	181 AlaciyThriysCysLeuValSerGlyTrpClyThrThriysSerProGlnValHisPhe 200 
GI:13169796	QY Dp	201 ProlysvalleughnCysleuAsnIleServalleuSerGhnLysArgCysGluAspAla 220
Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Qy . dd	221 TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer 240
rney, A.L.,	Oy	241 CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260 
wethod or prevoking the injury or death of retinal cells and treating ocular diseases Patent: WO 0109327-A 75 08-FEB-2001; Genentech, Inc. (US)	Qy da 1.	261 TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys 280 
LOCATION/QUAITITIES  /Organism="Homo sapiens" /mol_type="genomic DNA"	Oy	281 PheThrLysTrpileGlnGluThrileGlnAlaAsnSer 293 
424 g 329 t	RESULT 12 AX403421	
1.5e-120 Length: 1570 1608.00 Matches: 293 100.00% Maches: 0 100.00% Mismatches: 0 100.00% Indels: 0	LOCUS LOCUS ACCESSION VERSION KEYWORDS SOURCE ORGANISM	p DNA linear PAT 14-J 3454.
-936-271B-14 (1-293) x AX080829 (1-1570)	REFERENCE	Eukaljoraj metazoaj chologotaj vianigotaj veleblataj Eutheriaj Primates; Catarrhini; Hominidae; Homo.
	AUTHORS	Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,

	т 13 322	LOCUS AX464322 1570 bp DNA linear PAT 16-JUL-2002 DEFINITION Sequence 455 from Patent W00140466. ACCESSION AX464322 GI:21899177 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (burdata; Craniata; Vertebrata; Euteleostomi;	lini; Hominidae; Homo.	Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvarr Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurne Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C. Wood, W.L. and Zhang, Z.	TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same JOURNAL Patent: WO 0140466-A 455 07-JUN-2001; Genentech Inc. (US)	FEATURES Location/Qualifiers source 11570 /organism="Homo sapiens" /mol_type="genomic DNA"	T 332 a	1.5e-120 1608.00 100.00%	: 100.00% Mismatches: 100.00% Indels: 6 Gaps:	-09-936-271B-14 (1-293) x AX464322 (1-1570)  1 MetAlaThrAlaArgProProTrpMetTrpValLeuCysAlaLeuIleThrAlaLeuLeu 20	DD 554 ATGGCTACAGCAAGACCCCCTGGGATGTGGGGTGCTCTGTGTCTTGCTT 413  QY 21 LeuGlyValThrGluHisValLeuAlaAsnAsnAsnValSerCysAspHisProSerAsn 40  A11 CHILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	414 Ciococolocaconomicalicaconomicalication 47 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60	474 ACCGTGCCCTCTGGGAGCAACCAGGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGGTCG 53 61 AspaspSerSerSerArgIleIleAsnGlySerAspCysAspWetH1sThrGlnPrOTrp 80 111111111111111111111111111111111111	534 GATGACAGCAGCCGCATCATCAATGGATCCGACTGCGATATGCACACCCAGCCGTGG 59 81 GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro 10	Db 594 CAGGCCGCGCTGTTGCTAAGGCCCAACCAGCTCTACTGCGGGGCGGTGTTGGTGCATCCA 653  Qy 101 GlnTrpLeuLeuThralaAlaHisCysargLysValPheArgValArgLeuGlyHis 120	Db 654 CAGIGGCIGCICACGGCCGCCCACTGCAGGAAGAAGITICAGAGTCCGTCICGGCCAC 713
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z. TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same JOURNAL Patent: WO 0073454-A 308 07-DEC-2000; Geneticch Inc. (US) Geneticch Inc. (US) Location/Qualifiers 1. 1570 //mol_type="genomic DNA"	39 t	Alignment Scores: 1.5e-120 Length: 1570 Score: 1608.00 Matches: 293 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 6 Gaps: 0	US-09-936-271B-14 (1-293) x AX403421 (1-1570)	Qy 1 MetalathralaargProProTrpMetTrpValLeuCysAlaLeuLleThrAlaLeuLeu 20	Qy 21 LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn 40	Qy 41 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60	Qy 61 AspAspSerSerSerArgIleIleAsnGlySerAspCysAspMetHisThrGlnProTrp 80	Qy 81 GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro 100 	Qy 101 GlnTrpLeuLeuThrAlaAlaHisCySArgLysValPheArgValArgLeuGlyHis 120	Oy 121 TyrSerLeuSerProValTyrGluSerGlyGlnGlnWetPheGlnGlyValLysSerIle 140	Qy 141 ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 160	Qy 161 ArgarglleargProThrLysAspValArgProIleAsnValSerSerHisCySProSer 180	Qy 181 AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 200	Qy 201 ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla 220	Qy 221 TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer 240 	241 CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260

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Human kallikrein
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Hillman,J.L. and Lal,P.
Human kallikrein
Patent: US 5962300-A 2 05-007
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Qy 160		eArgProThrLysAs	pValArgProlleAsr	nArgArglleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSe	180
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5, 2003, 05:55:25; Search time 274 Seconds (without alignments) 2886.625 Million cell updates/sec OM protein - nucleic search, using frame\_plus\_p2n model US-09-936-271B-14 August Run on:

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	21	1608	00	1570	25	ABX64141	cDNA encoding huma
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	24	1513	94.1	1439	20	AAZ06260	Human secreted pro
	2,7	1002		11570	24	ABK30231 AAA95905	Human G-protein-co Human KLK-L2 gene.
	27	734		455	50	AAX57986	Human BS247 specif
U C	28	725		735	21	AAC79469 ABK29013	CDNA sequence of h
υo	30	725		738	50	AAX84240	
	31	688		673	22	AAF44901	breast
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	34	671		765	22	AAH85135	
	36.5	671		765	2 4 5	ABL95285 ACA59722	Human P/03P putati Prostate cancer th
	37	671		765	25	ABQ83343	encod
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	40	652.5		1146	20	AAV84589	a)
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	44	650.5	40.5	1106	200	AAZ22638 AAZ22639	12 nucleot
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RESULT AAZ233	ULT 1 23318	H 60					
8	A.	23318	standard;	DNA;	882	BP.	
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                            ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn
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Hodges SC, Klass MR, Kratochvil JD;
Yu H;
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97US-0063431
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Gordon J, Granados EN,
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28-OCT-1997;
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Russell JC,
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                                                                                                                                                                                                                                                                                                                 This invention describes a novel human prostate-derived serine protease
(PDSP) polynucleotide (also known as Tango 114). The prostate derived
serine protease (PDSP) polypeptide is used to modulate a variety of
cellular processes. It can used to produce fusion proteins. PDSP is used
to treat proliferative disorders, e.g. prostate cancer. The protein may
also be used to produce antibodies, end to identify antagonists and antibodies
can be used to produce antibodies, predictive medicine; and methods of
treatment. PDSP cleaves growth factors, and can be used for the
modulation of growth factor blosynthesis; generation of active peptides,
regulation of growth factor blosynthesis; queration of growth factor
binding proteins; regulation of cellular differentiation; regulation of
metastasis; and regulation of prostate development. The PDSP
metastasis; and regulation of prostate development; to detect PDSP mRNA;
to detect genetic alterations in the PDSP gene; in forensic biology; and
serine protease such as the prostate derived serine protease have important
relular processes, there exists a need for identifying novel
serine protease such as the prostate derived serine protease (PDSP) of
the invention. This sequence encodes the human PDSP-1 described in the
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                                                                                                                                                                                                                                                   . prostate derived serine protease polynucleotides and polypeptides to modulate cellular processes \boldsymbol{\cdot}
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 Homo sapiens
                            WO9946391-A2
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Sequence 1302 BP; 281 A; 413 C; 338 G; 270 T; 0 other;
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28-OCT-1997;
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Russell JC,
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                                                 This sequence is a BS247 specific polynucleotide.

The invention relates to a method of detecting the presence of a target BS247 polynucleotide, especially mRNA, in a test sample. BS247 polynucleotides are derived from breast tissue. The polynucleotides, polynucleotides are derived from breast tissue. The polynucleotides, polynucleotides are useful for providing information leading to the detection, diagnosis, staging, monitoring, prognosis, in vivo imaging, prevention or treatment, determining predisposition to, diseases and conditions of the breast, such as breast cancer, atypical hyperplasia, fibroadenoma and cystic breast disease. Drug treatment or gene therapy for breast cancer, can be based on these identified gene sequences and the efficacy of any particular therapy can be monitored. The BS247-derived reagents are advantageous for detection of breast cancer due to their specificity. The reagents also provide an alternative, non-surgical diagnostic method capable of detecting early stage breast disease, such as cancer.
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            consensus polypeptide sequence
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           tissue derived cDNA contig and
                                Claim 1; Page 105; 112pp; English.
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This sequence is a BS247 specific polynucleotide.

The invention relates to a method of detecting the presence of a target
The invention relates to a method of detecting the presence of a target
SS247 polynucleotide, especially mRNA, in a test sample. BS247
polynucleotides are derived from breast tissue. The polynucleotides,
polynucleotides are useful for providing information leading
to the detection, diagnosis, staging, monitoring, presponsis, in vivo
imaging, prevention or treatment, determining predisposition to, diseases
and conditions of the breast, such as breast cancer, atypical
on therapy for breast cancer, can be based on these identified gene
sequences and the efficacy of any particular therapy can be monitored.
The BS247-derived reagents are advantageous for detection of breast
cancer due to their specificity. The reagents also provide an
alternative, non-surgical diagnostic method capable of detecting early
stage breast disease, such as cancer.
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Granados EN, Hodges SC, Klass MR, Kratochvil JD;
, Stroupe SD, Yu H;
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AAZ06259 standard; DNA; 1381

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; ospitity edisorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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skin care product; skin flaking; dandruff; laundry detergent composition;
cleaning composition; dishwashing product; ss.
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                                         TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle
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                                                               GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This DNA encodes a human keratinocyte derived protease (KDP) polypeptide. The protease is substantially similar to a sequence encoded by the inserin plasmid FERM BP-6129. The KDP polypeptide, from human keratinocytes, is specifically used in skin care products, particularly to treat or prevent skin flaking, e.g. dandruff, and in laundry detergent compositions. More generally the KDP polypeptide can be used in any
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                                                          "keratinocyte derived protease"
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489..1169
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1..290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1499
                                                                                                                                                                               W09918219-A1
                                                                                                                                                                                                                                           03-OCT-1997;
                                                                                                                                                                                                                                                                         03-OCT-1997;
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ectides, based on which tissues they are most highly expressed in
                                                                                                       This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AA206210) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (nucleic acid sequences: AA206219-206263; amino acid sequences AAX08386-Y38498) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations the new polypuclocities. Specific uses are described for each of the 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AspAspSerSerArgIleIleAsnGlySerAspCysAspMetHisThrGlnProTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn
                                                         polypeptides they encode
                                                                                                                                                                                                                                                                                        BP; 338 A; 472 C; 381 G; 324 T; 1 other;
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293
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Matches:
Conservative:
Mismatches:
Indels:
 DR;
                                                           isolated human genes and the secreted
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Soppet
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                                                                                 Claim 1; Page 163-164; 227pp; English.
                                                                                                                                                                                                                                                                  (see AAZ06219 for described uses).
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 Rosen CA,
                       WPI; 1999-444190/37
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Best Local Similarity:
                                    P-PSDB; AAY38412
                                                                                                                                                                                                                                                                                        Sequence 1516
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 Olsen HS,
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                       TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle
                                                                       ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn
                                                                                                                       ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer
                                                                                                                                  CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer
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98US-0070658.
98US-0070692.
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 homologs and antibodies
           can be used in screening assays; predictive medicine; and methods of treatment. PDSP cleaves growth factors, and can be used for the modulation of growth factor biosynthesis; generation of active peptides; regulation of cellular proliferation; degradation of growth factor binding proteins; regulation of cellular differentiation; regulation of metastasis; and regulation of prostate development. The PDSP polynocleotides can be used to express the protein; to detect penetic alterations in the PDSP gene; in forensic biology; and as a source of primers and probes. As serine protease have important roles in cellular processes, there exists a need for identifying novel serine protease such as the prostate derived serine protease (PDSP) of the invention. This sequence encodes the human PDSP-1 described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
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293
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polypeptides,
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Mismatches:
Indels:
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polynucleotides,
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 The PDSP
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17-JUN-1998; 98US-0089538. 17-JUN-1998; 98US-0089598. 17-JUN-1998; 98US-0089599. 17-JUN-1998; 98US-0089600. 17-JUN-1998; 98US-0089653. 18-JUN-1998; 98US-0089801.	;;;; ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	6886			1,86	, ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;		, 66 98;			98;	, , , , , , , , , , , , , , , , , , ,	98;		, ; 8 6 6 6 7 6 8 6	, 68 98;	, 68 98;	, ; 60 8 ; 60 8 ;	, 60 , 60 , 60 , 60 , 60 , 60 , 60 , 60	, 86 98;		. 68	98;	, 86		, , , , , , , , , , , , , , , , , , ,		98;
PPRR																													
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TACCCGAACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACTCC CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer	TrpG1yAspTyrProCysAlaArgProAshAspProG1yVa1.	ZAI FRETRIJYSTIPLIEGINGIUTTILEGINALAASNSET 293 	RESULT 8 AAZ65070 ID AAZ65070 standard; cDNA; 1570 BP.	AAZ65070;	05-APR-2000 (first entry)	Membrane-bound protein PRO1132 encoding cDNA.	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.	Homo sapiens.	WO9963088-A2.	09-DEC-1999,	ж66 :666°	02-JUN-1998; 98US-0087607. 02-JUN-1998; 98US-0087609. 02-JUN-1908.	998; 9808 998; 9808	998; 980s	98; 98; 98; 98;	98; 980; 198; 980;	198; 98US	198; 9808 198; 9808	98; 9808	98;	98; 980s	98; 9808 98; 9808	198; 98US	98; 980	98; 980	98; 980	98;	98; 9808	980 980 980 980
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breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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                                                    1014 TACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys
ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer
                                                                                                                                                                GlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413
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Wood WI, Yuan J;
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Best Local Similarity:
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                                                 18-AUG-1998;
18-AUG-1998;
18-AUG-1998;
18-AUG-1998;
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16-SEP-1998;
12-JAN-1999;
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19-AUG-1998,
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  Mismatches:
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PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
Dolypeptide expression in a cell sample to that in a control sample.
Come of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in periorte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or
of T-lymphocytes, the release of a cytokine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
to factor VIIA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
PRO polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammallan tumours e.g. lung, breast, prostate, cervical
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Matches:
Conservative:
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99US-0170262.
99WO-US30095.
99WO-US30911.
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99WO-US28551.
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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P-PSDB; AAU12399.
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11-FEB-2000;
18-FEB-2000;
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22-FEB-2000;
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21-MAR-2000;
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10-NOV-2000;
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01-DEC-2000;
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06-JAN-2000;
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24-FEB-2000;
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(first entry)

02-APR-2001

Percent Similarity:

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Human; secreted and transmembrane protein; PRO; cytostatic;
cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                        Human PR01132 (UNQ570) nucleotide sequence SEQ ID NO:308.
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990S-01443048.
990S-0144758.
990S-0146298.
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2000WO-US03565
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2000WO-US07377
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                                                                                                                               diagnostic assay; ss
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P-PSDB; AAB65249.
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01-DEC-1999;
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20-DEC-1999;
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11-FEB-2000;
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26-JUL-1999;
28-JUL-1999;
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15-SEP-1999;
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8 \times 8
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Godowski PJ; Paoni NF; Wood WI;

proteins. The PROP proteins have evideatatic and transmeasurants from proteins. The PROP proteins have evideated ectivity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as can be used eat leach. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AFK44270 to AFK44470 represent PRO primers and hybridisation probes used in the isolation of human PRO sequences. AAF444087 to AAR65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention. The present invention describes human secreted and transmembrane PRO

Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other;

RESULT 11 ABK28605

1013 1073 240 473 593 100 653 120 140 773 160 833 180 893 200 953 260 413 533 40 9 80 21 LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn 61 AspAspSerSerArgIleIleAsnGlySerAspCysAspMetHisThrGlnProTrp GlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHis 654 CAGIGGCIGCICACGCCCCCCACIGCAGGAAGAAGIITITCAGAGTCCGICTCGGCCAC 141.ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 161 ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer 181 AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 201 ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer 1570 293 0 0 0 Matches: Conservative: Mismatches: Indels: Length: (1-1570)US-09-936-271B-14 (1-293) x AAF44216 2.07e-137 1608.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: 101 Query Match: .. oN . Pred g g ŏ g δλ ò a ò 셤 δ a ŏ 용 óγ ద δ g Qγ ŏ g ŏ g ò g δ g ŏ

BP

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ABK28605 standard; cDNA; 1570
                                                                                                                                                                             Wood WI;
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P-PSDB; AAU81966.
                                                                          WO200109327-A2.
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18-FEB-2000; 2
22-FEB-2000; 2
24-FEB-2000; 2
02-MAR-2000; 2
15-MAR-2000; 2
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Watanabe CK,
                                                                                                                                                                      Ashkenazi AJ,
                                                                  Homo sapiens.
                                                                                         28-JUL-2000;
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30-NOV-1999;
01-DEC-1999;
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06-JAN-2000;
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                                                                                 08-FEB-2001
       ABK28605:
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Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic; retinal cell injury; ocular disease; retinitis pigmentosa; macular degeneration; retinal detachment; retinal tear; retinopathy; retinal degenerative disease; macular hole; degenerative myopia; acute retinal necrosis syndrome; traumatic chorioretinopathy; Purtscher's retinopathy; oedema; ischaemic condition; retinal vision occlusion; collagen vascular disease; thrombocytopaenic purpura; uveitis; retinal vasculitis;Eales disease; systemic lupus erythematosus; environmental trauma.
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Hark MR, Marsters SA, Pitti RM;
                                                      Human DNA59767-1489 encoding PRO1132
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2000WO-US00219.
2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
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09-APR-2002 (first entry)
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Lafleur M,
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The invention relates to promoting the survival of retinal cells, or delaying or preventing retinal cell injury or death, by contacting the retinal cells with the polypeptide such as PRO175, PRO220, PRO216, PRO216, PRO316, Promoting survival of retinal cells, or delaying or preventing retinal cell injury or death, by contacting retinal cells with PRO175, 220, 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132 polypeptide Claim 33; Fig 28; 152pp; English.

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        degenerative myopi, acute retinal necrosis syndrome, traumatic chorioretinopathy occursion, Purtscher's retinopathy, oddema, an ischaemic condition, central or branch retinal vision occlusion, collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal vasculitis, occlusion associated with Eales disease or systemic lupus erythematosus), retinal injury or environmental trauma. The retinal cell injury or death is delayed or prevented by substantially not causing anglogenesis or mitogenesis. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                              354 ATGGCTACAGCAAGACCCCCCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTT
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 macular hole,
                                                                                                                      Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other;
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293
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                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
 retinopathy, retinal degenerative disease,
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                                                                                                                                                                                                            Gaps:
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1608.00
100.00%
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                                                                                                encoding a PRO protein.
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New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                   2000WO-US04114.
2000WO-US04914.
2000WO-US05004.
2000WO-US05601.
                   2000WO-US00277.
2000WO-US00376.
2000WO-US03565.
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2001US-0924419,
2001US-0927796,
2001US-0931836,
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2001WO-US06666.
2001WO-US17092.
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2001US-0808689.
2001US-0816744.
2001US-0828366.
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2001US-0854280.
2001US-0860216.
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2001US-0886342.
2001US-0887879.
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2001US-0866034.
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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P-PSDB; ABU66797.
          05-JAN-2000; 2
06-JAN-2000; 2
06-JAN-2000; 2
11-FEB-2000; 2
18-FEB-2000; 2
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  1074 TGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCC 1133
                                                                                                                                                                                             Human; PRO polypeptide, secreted and transmembrane protein;
tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder;
                                                        cDNA encoding human PRO polypeptide #228.
                                                                                                                  .ACA03830 standard; cDNA; 1570 BP
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98WO-US19093.
98WO-US19094.
98WO-US19177.
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99WO-US00106.
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17.SEP-1998
29.OCT-1998
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10-SEP-1998;
14-SEP-1998;
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Gao W;

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GCTGGGACAAAGTGCTTGGTGTCTGGCGGGACAACCAAGAGCCCCCAAGTGCACTTC
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inflammatory disease; organ failure; atheroscieroals; cardiac injury;
infertility; birth defects; premature aging; AIDS; biosensor;
acquired inmunodeficiency syndrome; cancer; diabetic complication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 455
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                                                    The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for inking bloactive molecules to cells expressing PRO polypeptides, and for for identifying agonists or antagonists.

The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TRF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic encoding the human PRO polypeptides, for generating transgenic animals or encoding the human PRO polypeptides of the invention.

Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at
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Conservative:
Mismatches:
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Claim 2; Fig 455; 660pp; English.
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The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid curder American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host calls for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, and the proliferation of differentiation of chondrocyte cells, the release of proteoglycans from cartilage, proliferation of inner ear urticular proteoglycans from cartilage, proliferation of inner are urticular proteoglycans from cartilage, proliferation of relaying the release of proteoglycans from propheral blood monouclear cells, the release of a cytokine from peripheral blood monouclear cells, the release of proteoglycans from peripheral blood monouclear cells, the release of a cytokine from peripheral blood monouclear cells, the release of proliferation of endothelial cells), a method for modulating the optimation of a tumour in a mammal and an oligonoucleotide probe derived from any of the nucleotide sequences cited above. The nucleic acids and cited above. The nucleic acids are useful as hybridisation of diabetic complications. Ald and an oligonoucleotide propertion probes, in chromosome and gene mapphag, and in generating antisense RNA or DNA. The polypeptides are useful as planmaceuticals, diagnostics, blosensors or blosensors or blosensors or blosensors are useful as PRO protein of the invention. New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature Gao W; DeForge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other; Length:
Matches:
Conservative:
Mismatches:
Indels: Claim 2; Fig 455; 659pp; English. 2.07e-137 1608.00 100.00% 100.00% Beresini M, aging, AIDS, or cancer Stewart TA, (GETH ) GENENTECH INC. WPI; 2003-331925/31. P-PSDB; ABU67073. Baker KP, Ber Gerritsen ME, Alignment Scores: Smith V, Pred. No.: 

354 ATGCCTACAGCAAGACCCCCCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTT 413

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US-09-936-271B-14 (1-293) x ACA04251 (1-1570)

Similarity:

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Gaps:

21 LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn

61 AspAspSerSerSerArgIleIleAsnGlySerAspCysAspMetHisThrGlnProTrp

41 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer

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              534 GATGACAGCAGCCGCATCATCAATGGATCCGACTGCGATATGCACACCCCAGCCGTGG
                                            GlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHis
                                                    TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle
                                                                                  241 CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer
                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel secreted and transmembrane protein PRO1132.
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Claim 2; Fig 455; 659pp; English.
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3 Gao s; Deforge L, Desnoyers L, Filvaroff E, A, Godowski PJ, Gurney AL, Sherwood S Tumas D, Watanabe CK, Wood WI, Zhang Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in included a broactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insulficiency disorders. PRO1164 and PRO1186 constituents are pro1186, pro828, pro828, pro826, pro828, pro826, p disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO813 and PRO11066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO814, PRO1312, PRO1192 and PRO1313 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This

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                                                                                                                                                                                      AspAspSerSerSerArgllelleAsnGlySerAspCysAspMetHisThrGlnProTrp
                                                                                                                                                                                              AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                       TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer
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              0 other;
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                                  Length:
Matches:
Conservative:
              BP; 332 A; 485 C; 424 G; 329 T;
                                                       Mismatches:
novel human PRO protein.
                                                               Indels:
                                                                                    US-09-936-271B-14 (1-293) x ABX89368 (1-1570)
                                                                     Gaps:
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Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth, c-fos induction; vascular endothelial growth inhibition; vEGF inhibition; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; chondrocyte redifferentiation; sports injury; arthritis; PCR; primer; ss.
                                                          Human secreted or transmembrane protein related PCR primer #56.
                  ABX80318 standard; DNA; 1570 BP
                                                                                                                                                                                                                98WO-US19330.
98WO-US19437.
98WO-US21141.
                                                                                                                                                                                                                                   99WO-US25108.
99WO-US00106.
99WO-US05028.
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                                             28-APR-2003 (first entry)
                                                                                                                                                                   US2002132252-A1.
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06-JAN-2000,
06-JAN-2000,
11 FEB-2000,
12-FEB-2000,
24-FEB-2000,
02-MAR-2000,
10-MAR-2000,
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15-MAR-2000,
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30-MAR-2000;
15-MAY-2000;
                                                                                                                                                       Homo sapiens.
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01-DEC-1999;
01-DEC-1999;
16-DEC-1999;
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16-SEP-1998;
17-SEP-1998;
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05-JAN-1999;
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15-SEP-1999;
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29-JUN-2001;
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22-MAY-2000;
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                               ABX80318;
    RESULT 15
ABX80318
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PR 16-UNN-1997; 971S-04978P
PR 12-NOV-1997; 971S-04578P
PR 12-NOV-1997; 971S-055260P
PR 12-NOV-1997; 971S-055260P
PR 12-NOV-1997; 971S-055311P
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PR 25-PEB-1998; 981S-078910P
PR 20-MAR-1998; 981S-078910P
PR 20-MAR-1998; 981S-078910P
PR 20-UNN-1998; 981S-07759P
PR 02-UNN-1998; 981S-07759P
PR 02-UNN-1998; 981S-07759P
PR 02-UNN-1998; 981S-081021P
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PR 11-UNN-1998; 981S-0P
PR 11-UNN-1998; 981S-0P
PR 11-UNN-1998; 981S-0P
PR 11-UNN-1998; 981S
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;

### WPI; 2003-247083/24.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments

# Example 99; Page 259; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO bolypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO

useful for treating cardiac insufficiency disorders. PRO1154 and PRO5186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO826, PRO1066, PRO943, PRO828, PRO828, PRO826, PRO943, PRO828, PRO828, PRO828, PRO828, PRO828, PRO828, PRO828, PRO8186 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375. stimulate proliferation of Estimulated T-lymphocytes and are therapeutically useful for tenhancing immune response. PRO826, PRO826, PRO1068 or PRO1132 enhances survival/proliferation of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO813 and PRO8106 induce proliferation of mammalian kidney mesangial cells, decreased mesangial cell function such as Berger disease or other rephyshology experience are useful for treating herbetiformis or Crohn's disease. PRO8131, PRO8132, pRO8132 induce the polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This sequence represents a primer used in the isolation of DNA encoding lovel human PRO polypeptides \$

Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other;

	. Length:	Matches:	Conservative:	Mismatches:	Indels:	. sure
	2.07e-137	1608.00	100.00%	100.00%	100.00%	25
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1570 293

US-09-936-271B-14 (1-293) x ABX80318 (1-1570)

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qq	354 ATGGCTACAGCAAGACCCCCCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTT	CACAGCCTTGCTT 413
δý	21 LeuGlyValThrGluHisValLeuAlaAsnAsnValSerCysAspHisProSerAsn	pHisProSerAsn 40
qa	414 CIGGGGGTCACAGAGCATGTTCTCGCCAACAATGATGTTTCCTGTGACCACCCTCTAAC	CCACCCTCTAAC 473
Qy	41 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyGluAspAlaArgSer	uAspAlaArgSer 60
qa	474 ACCGTCCCTTGGGAGCAACCAGGACTTGGGGAGCTGGGGCCGGGGAAGACGCCGGTCG	AGACGCCCGGTCG 533
Oy	61 AspAspSerSerArgllelleAsnGlySerAspCysAspWetHisThrGlnProTrp	SThrGlnProTrp 80
qq	534 GATGACAGCAGCAGCCATCATCAATGGATCCGACTGCGATATGCACACCCAGCCGTGG	CACCCAGCCGTGG 593
δλ	81 GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaV	LeuvalHisPro 100
q	594 CAGGCCGCGCTGTTGCTAAGGCCCAACCACTGTACTGCGGGGCGGTGTTGGTGCATCCA	STIGGIGCAICCA 653
ογ	101 GlnTrpLeuLeuThrAlaAlaHisCysArgLysValPheArgValArgLeuGlyHis	lArgheuGlyHis 120
qa	654 CAGTGGCTGCTCACGGCCGCCACTGCAGGAAGTTTTCAGAGTCCGTCTCGGCCAC	CCGTCTCGGCCAC 713
٥y	121 TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle	Wallysserile 140
qa	714 TACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGATGTTCCAGGGGGGTCAAATCCATC	GGTCAAATCCATC 773
Qy	141 ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn	ulleLysLeuAsn 160
qa	774 CCCCACCCTGGCTACTCCCACCCTGGCCACTCTAACGACCTCATGCTCATGCTCAAACTGAAAC	CATCAAACTGAAC 833
Qγ	161 ArgArgIleArgProThrLysAspValArgProileAsnValSerSerHisCysProSer	rHisCysProSer 180

834 AGAAGAATTCGTCCCACTAAAGATGTCAGACCCATCAACGTCTCCTCTCATTGTCCCTCT 893	181 AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 200	894 GCTGGGACAAAGTGCTTGGTCTCGGCTGGGGGGACAACCAAGAGCCCCCAAGTGCACTTC 953	201 ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla 220	954 CCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGGATGCT 1013	221 TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer 240	1014 TACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAGCAGGTAGAGACTCC 1073	241 CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260	1074 TGCCAGGGTGATTCTGGGGGGCCTGTGGTTTGTTTTTTTT	261 TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys 280	1134 TGGGGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAG 1193	281 PheThrLysTrp1leGlnGluThr1leGlnAlaAsnSer 293	
83	18	88	20	95	22	101	24	107	26	113	28	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### 2, Appli 2, Appli 2, Appli 1, Appli 94, Appl , App Appli Appli Appli Appli Sequence 308, App Appl Description Sequence Sequence Sequence Sequence Sequence 5 Sequence 5 Sequence 1 Sequence 2 Sequence 7 Sequence 2 Sequence 2 US-09-996-243-308 US-08-824-874-2 US-09-210-084-2 US-09-280-116-1 US-09-280-116-1 US-09-280-116-1 US-09-386-642-10 US-09-386-642-10 US-09-205-258-247 US-08-944-483-7 US-08-944-483-7 US-08-944-483-7 SUMMARIES DB Query Match Length 999.2 999.2 897.3 87.3 440.7 440.6 440.6 40.5 100.0 652.5 652.5 650.5 650.5 Score 1403 Result No.

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		639.5	39.8	994	m	US-09-008-271A-19	19,
-		638.5	39.7	944	e	US-09-070-526-1	1,
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		638	39.7	871	e	US-09-261-767-2	7
		638	39.7	871	4	6 - 696	Sequence 7, Appli
		638	39.7	1248	٣	US-09-020-956-171	171
		638	39.7	1248	٣	9-030-60	171,
		638	39.7	1248	4	US-09-439-313-171	171,
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	35	612.5	38.1	986	7	US-08-557-146-1	Sequence 1, Appli
	36	612.5	38.1	986	7	US-09-154-344-1	Ä
ပ	.37	612.5	38.1	1089	m	US-08-930-188-1	'n
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### ALIGNMENTS

RESULT 1

				•																								Polypeptides and Nucleic			•			
3-308	Sequence 308, Application US/09996243	6478825	FORMATION:	: Ashkenazi, Avi J.	: Baker, Kevin P.	: Botstein, David	: Desnoyers, Luc	: Eaton, Dan L.	: Ferrara, Napoleone		: Gerber, Hanspeter	: Gerritsen, Mary E.	: Goddard, Audrey	: Godowski, Paul J.	: Grimaldi, J. Christopher			: Napier, Mary A.	: Pan, James	: Paoni, Nicholas F.			: Tumas, Daniel		٠.		: Zhang, Zemin	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	TITLE OF INVENTION: Acids Encoding the Same	FILE REFERENCE: P2730P1C13	PPLICATION NUMBER: US/09/996,243	CURRENT FILING DATE: 2001-11-14	PRIOR APPLICATION NUMBER: 60/049787	PRIOR FILING DATE: 1997-06-16
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4	1997-10-17	NUMBER: 6U/065186 1997-11-12	NUMBER: 60/065311	1997-	1997-11-24	NUMBER: 60/075945	NUMBER: 60	1998-03-20	NUMBER: 00/083322 1998-04-28	NUMBER: 60	L998-05-0 NUMBER: 60	1998-05-28	NUMBER: 60/087607 1998-06-02	NUMBER: 60	1998-06	1998-06-02	NUMBER: 60	NUMBER: 6	1998-	1998-06-04	NUMBER: 60	NUMBER: 60	1998-06 NUMBER:	1998-06-04	NUMBER: 60/088030 1998-06-04	NUMBER: 60	NUMBER: 60	1998- NUMBER	1998-06-05	NUMBER: 60/088202 : 1998-06-05	NUMBER: 60	NUMBER: 60	1998-06-0 NUMBER: 60	1998-06-09	1998-06-10	NUMBER: 60 1998-06-1	NUMBER: 60	NUMBER: 60	1998-06	1998-06-10	NUMBER: 60/088826	NUMBER: 60	1998-06-11 NIMBER: 60/088861	1998-06-11	₽⊓	NUMBER: 60	1998-06-12 NUMBER: 60/089440
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AFFILING DATE: 1998-UD-LD
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APPLICATION NUMBER: 60/090472
TIVE DATE: 1998-06-24 FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 CATION NUMBER: 60/089599 APPLICATION NUMBER: 60/089653 60/089801 APPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/089948 APPLICATION NUMBER: 60/089952 60/090246 60/090252 60/090349 60/090355 APPLICATION NUMBER: 60/090429 APPLICATION NUMBER: 60/090431 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090557 9/9060/09 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/089598 60/089947 APPLICATION NUMBER: 60/090254 60/090694 1998-06-24 1998-06-18 1998-06-19 1998-06-23 FILING DATE: 1998-06-24 1998-06-25 1998-06-17 1998-06-17 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/ 1998-06-22 1998-06-22 1998-06-24 1998-06-24 998-06-24 1998-06-25 1998-06-17 998-06-2 :-90-866 7-90-8661 -90-8661 APPLICATION NUMBER: APPLICATION NUMBER:

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954 CCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGGATGCT 1013
                               Length:
Matches:
Conservative:
Mismatches:
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APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.(
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                      US-08-824-874-2; Sequence 2, Application US/08824874; Patent No. 5962300; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CLONE: 820694
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Best Local Similarity:
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Matches:
Conservative:
Mismatches:
Indels:
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                          PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091636
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091631
PRIOR APPLICATION NUMBER: 60/091631
PRIOR APPLICATION NUMBER: 60/091631
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
APPLICATION NUMBER: 60/090863
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                   DATE: 1998-06-26
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Best Local Similarity:
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oGinTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHi 120
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Indels:
                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 |
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
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1595.00
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                                              : Diskette
IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 1476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                   COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity:
Palo Alto
                    USA
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                    COUNTRY:
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                                                                                        ThrvalProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60
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          MetalaThralaArgProProTrpMetTrpValLeuCysAlaLeuIleThrAlaLeuLeu
                             277 ATGCTACAGCAAGACCCCCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTT
                                                LeuGlyValThrGluH1sValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-210-084-2
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; LIBRARY: KERANOT02 ; CLONE: 820694 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-764-762-2 Alignment Scores: 2.12e-159 Length: 1476 Score: 1595.00 Matches: 293 Percent Similarity: 99.66% Conservative: 0 Best Local Similarity: 99.66% Mismatches: 0 Ouery Match: 4 Gaps: 0 US-09-936-271B-14 (1-293) x US-09-764-762-2 (1-1476)	Qy 1 MetalatralaargProProTrpMetTrpValLeuCysAlaLeuIleThrAlaLeuLeu 20	Qy 21 LeuGlyValThrGluHisValLeuAlaAsnAspValSerCysAspHisProSerAsn 40	Qy 41 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60	Qy 61 AspaspSerSerargIleIleAsnGlySerAspCysaspMetHisThrGlnProTrp 80	Qy 81 -GinalaalaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPr 100	Qy 100 oGlnTrpLeuLeuThrAlaAlaHisCysArgLysValPheArgValArgLeuGlyHi 120	Qy 120 sTyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIl 140	Qy 140 eProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAs 160	Qy 160 nArgArg11eArgProThrLysAspValArgPro1leAsnValSerSerHisCysProSe 180	Qy 180 ralaGlyThrLysCysLeuValSerGlyThrGlyThrThrLysSerProGlnValHisPh 200	Qy 200 eProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAl 220	Qy 220 aTyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSe 240	Oy 240 rcysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSe 260	Qy 260 rTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLy 280	Qy 280 sPheThrLysTrp11eGlnGluThr11eGlnAlaAsnSer 293
	Qy 220 aTyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSe 240	Qy 240 rCysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSe 260 	Qy 260 rTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrasnLeuCysLy 280	Qy 280 sPheThrLysTrpIleGlnGluThrIleGlnAlaAsnSer 293 	RESULT 4 US-09-764-762-2 ; Sequence 2, Application US/09764762 . Datort M. 6477105	GENERAL INFORMATION:  APPLICANT: Hillman, Jennifer L.  Lal, Preeti	TITLE OF INVENTION: NOVEL KALLIKREIN  NUMBER OF SEQUENCES: 5  CORRESPONDENCE ADDRESS:  ADDRESSEE: Incyte Pharmaceuticals, Inc.	STATE: CA CUNTRY: USA	EADAU	CURRENT APPLICATION DATA:  CURRENT APPLICATION DATA:  APPLICATION WHORER: US/09/764,762	FILING PAREL TO DATE TO UNIT THE UNIT TO UNIT THE UNIT TH		TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEPHONE: 415-845-4166	SEQUENCE CHARACTERISTICS:  TYPE: nucleic acid  CHARACTERISTICS:	TOPOLOGY: linear : IMMEDIATE SOURCE:

1056

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275

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216 ArgCysGluAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLys
                                       ArgProThrLySASpValArgProIleAsnValSerSerH1sCysProSerAlaGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                734 CGTCCCACTAAAGATGTCAGACCCATCAACGTCTCCTCTCTTGTCCCTCTGCTGGACA
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                                                                                                                                                      293
                                                                                                                                                    275 rThrAsnLeuCysLysPheThrLysTrpIleGlnGluThrIleGlnAlaAsnSer
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE T
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 21012.14465
CURRENT REPERENCE: 2000-06-22
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 94
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-936-271B-14 (1-293) x US-09-602-877A-94 (1-735)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                     US-09-602-877A-94/c
; Sequence 94, Application US/09602877A
; Patent No. 64312/07
; GENERAL INFORMATION:
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725.00
100.00%
100.00%
45.09%
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                 Human Protease Homologs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nThr-ValProSerGlySer-AsnGlnAspLeuGlyAla---GlyAlaGlyGluAspAla
 GTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC 1156
                                                                                                                                                                                                                                   1504
280
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12
                                                                                 Encoding
                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-1
                                                                                                                                                                                                                                                                                                        US-09-936-271B-14 (1-293) x US-09-280-116-1 (1-1504)
                                                                  APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules I
FILE REFRENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SCFTWARE: Patentin Ver. 2.0
                                         US/09280116A
                                                                                                                                                                                                                                   4.79e-139
1403.00
93.778
91.808
87.258
                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                            US-09-280-116-1
; Sequence 1, Application
; Patent No. 6331427
                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                            GENERAL INFORMATION:
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Pred. No.:
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                                                                                                                                                                                          19 LeuLeuLeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisPro
                                                 161 ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer
                                                                        GAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACC
                                                                                                                                                                                                                                                                                                                           240 SerCysGlnGlyAspSerSlyGlyProValValCysAsnGlySerLeuGlnGlyLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                           260 SerTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 SerAsnThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAla
                                                                                                                                                                                                                                                                TyrProArgGlnIleAspAspThrMetPheCysAla---GlyAspLysAlaGlyArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene; OTHER INFORMATION: with homo sapien serine protease catalytic domain US-09-386-642-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 LysPheThrLysTrpIleGlnGluThrIleGlnAlaAsn 292
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Darrow, Andrew
APPLICANT: Oi. Jenson
APPLICANT: Oi. Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT APPLICATION NUMBER: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
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Sequence 10, Application US/09386642

Patent No. 6420157

; GENERAL INFORMATION:
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Best Local Similarity:
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250 CACAGTCTTGAGGCCGACCAAGAGCCAGATGGTGGAGGCCAGCCTCTCCGTA 309
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CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-936-271B-14 (1-293) x US-09-439-313-524 (1-765)
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Indels:
                             Length:
Matches:
            284 TrpileGlnGluThrileGlnAlaAsnSer
                                                                                                                                                                    APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan Louise APPLICANT: Jiang Yuqui APPLICANT: Reed, Steven G. APPLICANT: Kalos, Michael
                                                                                                                  Sequence 524, Application US/09439313
Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.11e-62
671.00
61.778
45.738
41.738
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                                                                                                                                                                                                                                                                                              Fanger, Gary
Retter, Mark
Solk, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-524
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Best Local Similarity:
Query Match:
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                                                                                                 US-09-439-313-524
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EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 247
LENGTH: 1146
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   R APPLICATION NUMBER: 60/048,900
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,901
R APPLICATION NUMBER: 60/048,892
R FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,373
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,875
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,897
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,898
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,992
                                                                                                       R FILING DATE: 1997-06-06

A PPLICATION NUMBER: 60/048,884

R FILING DATE: 1997-06-06

A PPLICATION NUMBER: 60/048,894

R FILING DATE: 1997-06-06

A PPLICATION NUMBER: 60/048,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/048,970
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,972
ELING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/048,917 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,949
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APPLICATION UNBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
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PILING DATE: 1997-06-06
PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,877
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APPLICATION WUMBER: 60/048,878
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/070,923
                                                                                                                                                                                                                                      FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,882
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/048,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/049,019
FILING DATE: 1997-06-06
                  FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
                                                           FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,895
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/048,899
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436 ATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACC 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyValTyrThrAsnLeuCysLysPheThrLysTrpIleGlnGluThrIleGlnAlaAsn 292
                                                                                       98 ValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArg 117
                                                                                                                                                                                                                                           118 LeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyVal 137
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319 CTGGGGCAGCACAACCTCCAGAAG---GAGGAGGCTGTGAGCAGACACCCGGACAGCCACT 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 GlnLysArgCysGluAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGly 233
142 GCCCCCTTTGATGATGATGACAAGATCGTTGGGGGGCTACAACTGTCTAGAAAAGCACTCC 201
                                                                GlnProTrpGlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeu 97
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US'88/11422
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 247, Application US/09205258 Patent No. 6525174 GENERAL INFORMATION:
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|TCT 858
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APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
UNUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                              261 TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys
 222 ProArgGlnIleAspAspThrMetPheCysAlaGly---AspLysAlaGlyArgAspSer
                                                                                                                                                                                                                                    281 PheThrLysTrplleGlnGluThrlleGlnAlaAsn 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSED for Windows Version 2.0 CURRENT APPLICATION DATA:
FILLING DAMPS: US/08/944 402
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                                                                                                                                                                                                                                                                                                                     ; Sequence 7, Application US/08944483
; Patent No. 6232456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Abbott Laboratorie
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 611
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/936-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: RUSSELL, JOHN C. APPLICANT: STEWART, KENT D.
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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68.67%
50.64%
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: single
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 ITCGAGAAGACGCGGCTACTCTGTGGGGCGACGCTCATCGCCCCCAGATGGCTCCTGACA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHisTyrSerLeuSerPro 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 GCAGCCCACTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GAGGAGGCTGTGAGCAGACCGGACAGCCACTGAGTCCTTCCCCCACCACCGGCTTC 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 GlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhePro 201
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US-09-205-258-247
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                                                                     equals a,t,g,
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652.50
57.88%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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OTHER INFORMATION:
                                                                    OTHER INFORMATION:
                                                                                                       SITE
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NAME/KEY: SITE
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LOCATION:
                                                                                  FEATURE:
NAME/KEY:
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OTHER INF
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                                                                                                                             LeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisProGlnTrpLeuLeu 104
                                                                                                                                                                                       ThralaalaHisCysArgLysLysValPheArgValArgLeuGlyHisTyrSerLeuSer 124
                                                                                                                                                                                                                                                                                                                                   394 TTCAACAACAGCCTCCCCAACAAGACCACCGCAATGACATCATGCTGGTGAAGATGGCA 453
                                                                                                                                                                                                                                                                ACAGCAGCCCACTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                 574 CCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAGAACGCC
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                                                                      SerArgIleIleAsnGlySerAspCysAspMetHisThrGlnProTrpGlnAlaAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08790137
Patent No. 5840871
GENERAL INFORMATION
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
TITLE OF INVENTION: A LIKREIN
NUMBER OF SEQUENCES: 4
                                         US-09-936-271B-14 (1-293) x US-08-944-483-7 (1-1166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
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MEDIUM TYPE: Diskett
COMPUTER: IBM COMPAT
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128 GluSerGlyGlnGlnMetPheGlnGlyValLysSerIleProHisProGlyTyrSer--- 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 ------HisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsnArgArgIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 LeuAlaAsnAsnAspValSerCysAspHisProSerAsnThrValProSerGlySerAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 IleAsnGlySerAspCysAspMetHisThrGlnProTrpGlnAlaAlaLeuLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 ProAsnGlnLeuTyrCysGlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 CACTGCCTNAAGCCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAAG---GAG
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43
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                     7.0
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Matches:
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DOS
for Windows Version
                  SOFTWARE: FastSEQ for Windows Ver
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/790,137
FILING DATE: Filed Herewith
                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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58.628
43.798
                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 833 base pairs
TYPE: nucleic acid
                                                                                FILING DATE: Filed He CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             linear
    OPERATING SYSTEM:
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                                                                                                                                                                FILING DATE:
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US-08-790-137-2
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65 67 163

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerCysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT 856
                                          Conservative:
                                                                                                                                                  US-09-936-271B-14 (1-293) x US-08-944-483-8 (1-1192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
                                                                Mismatches:
  Length:
Matches:
                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 189, Application US/09205258 Patent No. 6525174 GENERAL INFORMATION:
1.78e-59
650.50
68.24%
50.64%
                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-205-258-189
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APPLICATION NUMBER: 60/048,963 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,877 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,915 PLICATION NUMBER: 60/049,019 LING DATE: 1997-06-06 LING DATE: 1997-06-06
PLICATION NUMBER: 60/048,970 FILLING DATE: 1997-06-06 APPLICATION NUMBER: 60/049,373 APPLICATION NUMBER: 60/048,875 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,883 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,898 PILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,962 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,878 FILING DATE: 1997-06-06 PLICATION NUMBER: 60/070,923 LING DATE: 1997-12-18 APPLICATION NUMBER: 60/049,375 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,896 APPLICATION NUMBER: 60/049,020 APPLICATION NUMBER: 60/048,895 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,884 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,899 APPLICATION NUMBER: 60/048,893 APPLICATION NUMBER: 60/048,900 PLICATION NUMBER: 60/048,892 PLICATION NUMBER: 60/048,972 PLICATION NUMBER: 60/048,916 APPLICATION NUMBER: 60/049,374 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,949 APPLICATION NUMBER: 60/048,881 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,880 APPLICATION NUMBER: 60/048,882 PLICATION NUMBER: 60/048,901 APPLICATION NUMBER: 60/048,917 APPLICATION NUMBER: 60/048,897 APPLICATION NUMBER: 60/048,876 APPLICATION NUMBER: 60/048,894 APPLICATION NUMBER: 60/048,971 APPLICATION NUMBER: 60/048,964 APPLICATION NUMBER: 60/092,921 1997-06-06 FILING DATE: 1997-06-06 1997-06-06 FILING DATE: 1997-06-06 1997-06-06 1997-06-06 1997-06-06 1997-06-06 FILING DATE: 1997-06-06 LING DATE: 1997-06-06 LING DATE: 1997-06-06 1997-06-06 1997-06-06 LING DATE: 1997-06-06 LING DATE: 1997-06-06 FILING DATE: 1997-06-06 FILING DATE: 1997-06-06 1997-06-06 1997-06-06 FILING DATE: FILING DATE: FILING DATE: LING DATE: FILING DATE: LING DATE: FILING DATE: LING DATE: LING DATE: EARLIER REARLIER EARLIER I EARLIER I EARLIER I EARLIER EARLIER

381 ACAGCAGCCCACTGCCTCAAGCCCCGGTACATAGTTCACCTGGGGCAGGACAACCTCCAG 440 161 ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer 180 181 AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 200 ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla 220 858 TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGC 917 LeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisProGlnTrpLeuLeu 104 125 ProvalTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIleProHisProGly 144 441 AAG---GAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAGTCCTTCCCCCACCCGGC 497 105 ThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHisTyrSerLeuSer 124 65 SerArgilelleAsnGlySerAspCysAspMetHisThrGlnProTrpGlnAlaAlaLeu TyrProArgGlnIleAspAspThrMetPheCysAlaGly---AspLysAlaGlyArgAsp SerTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCys 1292 118 41 67 280 LysPheThrLysTrpIleGlnGluThrIleGlnAlaAsn, 292 US-09-936-271B-14 (1-293) x US-09-205-258-189 (1-1292) Conservative: Mismatches: Indels: Gaps: Length: Matches: EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PALENTIN VER. 2.0
SEQ ID NO 189
LENGTH: 1292 2.01e-59 650.50 68.24% 50.64% TYPE: DNA COCANISM: Homo sapiens US-09-205-258-189 Percent Similarity: Best Local Similarity: Query Match: Aliqnment Scores: 221 240 201 260 82 678 738 798 Pred. No.: QQ ò g ò g ò g ò g ò 엄 δ g ô g ò g ŏ

797

; Sequence 2, Application US/09025059; Patent No. 6075136

RESULT 14 US-09-025-059-2

814 259

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161 ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer 180
                                                                                         181 AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 200
                                                                                                                                                                                                                                                                                                                                      260 SerTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCys 279
                                                                                                                                                                                                                                                                                                                                                                                                                    ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla
                                                                                                                                                                                                          695 CCTCACACACCTTGCGATGCGCCAACATCACCATTGAGCACCAGAAGTGTGAGAACGCC
                                                                                                                                                                                                                                                                                                                     240 SerCysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuVal
                                                                                                                                                                                                                                               TyrProArgGlnIleAspAspThrMetPheCysAlaGly---AspLysAlaGlyArgAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IDE COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
OF INVENTION: HUMAN PROTEASE MOLECULES
OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: <Unknown>FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mohan-Peterson, Sheela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bandman, Olga
Hillman, Jennifer
Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 19
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 TTCAACAACAGCCTCCCCAACAAGACCACCGCAATGACATCATGCTGGTGGAGGATGGCA 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 AAG---GAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAGTCCTTCCCCCACCCGGC
                   APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-936-271B-14 (1-293) x US-09-025-059-2 (1-1314)
                                                                                                                                                                                                                                                                              SOFTWARE: FastSEG for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                              3: Incyte Pharmaceuticals, Inc 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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50.64%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                 STREET: 3174 Por
CITY: Palo Alto
STATE: CA
GENERAL INFORMATION:
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Best Local Similarity:
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126
43
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7
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                  US-09-936-271B-14 (1-293) x US-09-008-271A-19 (1-994)
TOPOLOGY: linear

TOPOLOGY: linear

LIBMEDIATE SOURCE:

LIBMARY: COLNNOT27

CLONE: 1798496

SEQUENCE DESCRIPTION: SEQ ID NO: 19
US-09-008-271A-19
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639.50
57.09%
42.57%
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